



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102238

TO: Minh-Tam Davis
Location: CM-1/8A01/8E12
Art Unit: 1642
Thursday, August 28, 2003

Case Serial Number: 09/554945

From: Mary Jane Ruhl
Location: Biotech-Chem Library
CM1-6A06
Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes

Examiner Davis,

Here are the results for your recent search request.

sgt/28

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
CM-1, Rm. 6-A-06
605-1155

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RESULT 9
RNSGIII

LOCUS RNSGIII 2146 bp mRNA linear ROD 07-DEC-1994
 DEFINITION Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.
 ACCESSION U02983
 VERSION U02983.1 GI:413765
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 2146)
 AUTHORS Dopazo A., Lovenberg, T.W., Danielson, P.E., Ottiger, H.P. and
 Sutcliffe, J.G.
 TITLE Primary structure of mouse secretogranin III and its absence from
 deficient mice
 JOURNAL J. Mol. Neurosci. 4 (4), 225-233 (1993)
 MEDLINE 95001263
 PUBMED 7917832
 REFERENCE 2 (bases 1 to 2146)
 AUTHORS Dopazo, A.
 TITLE Direct Submission
 JOURNAL Submitted (28-OCT-1993) Dopazo A., The Scripps Research Institute,
 Molecular Biology, 10666 N. Torrey Pines Rd., La Jolla, CA 92037,
 USA

FEATURES
 source Location/Qualifiers
 1..2146
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
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 RISEANDRQVDFQKIVYSLKLNLTDEYSTGSLDQVDDPGLHQDGLDPLAEADIVHKIAT
 TQENTNODKIPKTPVPAQTNRENDTNTVNTLTSLNGLRRNPHRDDDFEE
 LQVFNFPALLTSIDSEKAKKEGTITMTKLIDFVKMWVYKGTISPBGYSYLENL
 DETIALQTNKLEKTTDSKLFPAPEKSHETDSTKEAAKKEVGSUKDSTKD
 DSNLGGKCTDEAKTEAYLEALRIENIWLKHKHKNKEDYDLSKMRDPINQADAY
 VEGILDKEENAINRIYSSSL"
 BASE COUNT 691 a 523 c 496 g 436 t
 ORIGIN
 Query Match 60.6%; Score 1221.6; DB 10; Length 2146;
 Best Local Similarity 79.4%; Pred. No. 2.2e-250;
 Matches 1584; Conservative 0; Mismatches 370; Indels 41; Gaps 10;
 Qy 1 TAAAGCTAGCGCTGGCGGAGTCTCC--CGGTACAGGAACCTTCAGCACCCACAGCGCG 58
 Db 9 TAAAGCTACCCCGAGCGCGGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 68
 Qy 59 GACAGCGCTCCCTCTACCTGGAGACTTGACTCCCGCGCGCCCAACCCCTGCTTAFCCCT 118
 Db 69 GACAGCGCGCGCGACCTGCTCACCTGCTCCGGCGCGGAGAGAGGAGGAGGAGGAGGAG 128
 Qy 119 TGACCGTCTGAGTGTCTAGAGATCTGACGCGCGCCAGTCCGCGCGCCCTCTCCGCGCCCA 178
 Db 129 CCAGCGCGCTGAGACTGCCACCGCGCGCG-----CCAGATCTCTCCCTTCTCTGCA 181
 Qy 179 CCACCTCTCTGCTCTTCTGTTTTTACTCTCTCTTTTCATTATCAAAAGCTACAG 238
 Db 182 CCCAGGCTCTGTCCTTCCAGTCTTACTCTCCCTCTCTATTCATTCAAAAGCTACAG 241
 Qy 239 CTCAGGAGCCAGCGCGCGGTGT-----GACCCAGCGGAGCGGCGGAGGAGGAGGAGG 290
 Db 242 CT-CAGGGGCCAGCGCCAGCTCTTCCAGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGG 300
 Qy 291 GTTCTCTGGGACCGGCACTTGGATCTGGTGTTAGTGCT-----CCGATTCAGAC 341
 Db 291 GTTCTCTGGGACCGGCACTTGGATCTGGTGTTAGTGCT-----CCGATTCAGAC 341

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 08:23:38 ; Search time 70 Seconds
(without alignments)
1061.201 Million cell updates/sec

Title: US-09-554-945b-2

Perfect score: 2402

Sequence: 1 MGFLGTGTWILVLPQAF.....EKGILDKKEAEAIRKRIYSSL 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2402	100.0	468	21	AA1985
2	2384	99.3	468	21	AA1981
3	2384	99.3	468	22	AA1982
4	2384	99.3	468	22	AA1983
5	2384	99.3	468	23	AA1984
6	2384	99.3	468	24	AA1985
7	2384	99.3	468	24	AA1986
8	2384	99.3	468	24	AA1987
9	2384	99.3	468	24	AA1988

10	2384	99.3	468	24	ABU72183	Human PRO polypept
11	2384	99.3	468	24	ABU66614	Human PRO polypept
12	2384	99.3	468	24	ABU66890	Human secreted/tra
13	2384	99.3	468	24	ABU59695	Novel secreted and
14	2384	99.3	468	24	ABG73287	Human neurosecret
15	2384	99.3	567	22	AAO13905	Human polypeptide
16	2377	99.0	468	22	AAAG3910	Human polypeptide
17	2289	95.3	470	22	ABG12976	Novel human diagno
18	2093.5	87.2	471	23	ABBS7046	Mouse ischaemic co
19	1989	82.8	396	24	AAO16322	Human secreted pro
20	597	24.9	316	22	ABG14006	Novel human diagno
21	472	19.7	212	22	ABG14003	Novel human diagno
22	182	7.6	665	21	ABAB18278	Plasmodium falcipa
23	173.5	7.2	1881	23	ABP73809	Candida albicans e
24	173	7.2	1099	19	AAW40538	Mutant C-beta prot
25	173	7.2	1558	21	AAAB18324	Plasmodium falcipa
26	173	7.2	1786	18	AAW24790	P. falciparum live
27	173	7.2	1787	23	AAU96699	Plasmodium falcipa
28	172.5	7.2	1979	21	AAAB18171	Plasmodium falcipa
29	172	7.2	493	13	AAAB26944	P.falciparum ISA g
30	172	7.2	1164	19	AAW40537	Group B streptococ
31	171	7.1	1093	19	AAW40540	Mutant C-beta prot
32	169.5	7.1	1164	17	AAAR83781	Group B Streptococ
33	169.5	7.1	1164	21	AAAY84459	Amino acid sequenc
34	169.5	7.1	1392	20	AAAY06999	Restin protein seq
35	169	7.0	1129	21	AAAY84462	Amino acid sequenc
36	168	7.0	1164	19	AAW40541	Mutant C-beta prot
37	168	7.0	1164	21	AAAY84463	Amino acid sequenc
38	168	7.0	1254	11	AAAR07503	Merozoite apical-en
39	168	7.0	1254	18	AAW24575	Merozoite apical-e
40	167	7.0	1427	12	AAW10534	Human 160kD mediat
41	166	6.9	1128	19	AAW40539	Mutant C-beta prot
42	166	6.9	1128	21	AAAY84461	Amino acid sequenc
43	165.5	6.9	1788	22	ABE62995	Drosophila melanog
44	165	6.9	1135	21	AAAY84460	Amino acid sequenc
45	163	6.8	309	22	ABG12975	Novel human diagno

ALIGNMENTS

RESULT 1
AA1985
ID AA1985 standard; Protein; 468 AA.

XX AA198555;

XX 07-JUL-2000 (first entry)

XX Human HsgIII protein.

XX Human; secretogranin; HsgIII; NPCABC08 protein; SgIII family; cancer;

XX leukaemia; diabetes mellitus; kidney disease; autoimmune disease;

XX diagnosis; therapy.

XX Homo sapiens.

XX WO200017349-A1.

XX 30-MAR-2000.

XX 22-SEP-1998; 98WO-CN00199.

XX 22-SEP-1998; 98WO-CN00199.

XX (UYSH-) UNIV SHANGHAI SECOND MEDICAL.

XX Chen J, Fu G, Song H;

XX WPI; 2000-283577/24.

XX N-PSDB; AAA07414.

XX New NPCABC08 polypeptide comprising a 468 amino acid sequence, useful

in the treatment of cancer, leukaemia, diabetes mellitus, kidney disease and autoimmune disease -

Claim 1; Page 22; 33pp; English.

This sequence is the human HsgIII protein of the invention. The protein is also referred to as the NPCABC08 polypeptide, and is a member of the secretogranin III (SgIII) family of polypeptides. The DNA and protein sequences are useful in the treatment of cancer, leukaemia, diabetes mellitus, kidney disease and autoimmune disease. They are also useful in detecting diseases associated with inappropriate NPCABC08 activity or levels.

Sequence 468 AA;

very Match
100.0%; Score 2402; DB 21; Length 468;

Best Local Similarity 100.0%; Pred. No. 1,6e-146;

Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MGFLGTWILVLPPIQAFPKPGSODKSLHNRELSAERPLNEOTAFAEEDKTKKTYPP 60

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61 ENKPGOSNYSEVDNI.NI.L.BAITEKEKIEKEBOSIBSSDIPDKNI NVEEDVETNBYI IDBY 120

121 DSTKSGI.DHKEDDDPDCI HQI DCTPI EAEEDTVHYTAAADIVSENDQSVUTDKYTHCKYT... 100

121 PSTKSGI.DHKEODRDCI.HAI.DCTPI.TAEEDTUVH.TA.DIUTENDR.DVUTRKY.TN.O

181 ITESQAHTI EREVA EVI OKI TSEANINVEEDNEDETCIMNOC OKEDEEM... 0.0

181 ITESCAHMY EDEUAEVY OZI TCZTANNUEDOCNOCOTRAC

CALIFORNIA STATE BAR ASSOCIATION

[illegible][illegible][illegible]

----- PARTIAL RELEASE OF INFORMATION ACT -----

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[illegible]

421 RUDRRKRNKREDIDPSRMNDFINNQADAI VERGILDKEEAEAIKRIYSSL 468

T 2

520
AAB18926 standard; Protein: 468 AA.

AAB18926:

08-FEB-2001 (first entry)

A novel polyimide designated PPO5000

SECRET

PRO1889; PRO1890; PRO1887; PRO1785; PRO4353; PRO4357; PRO4405; PRO4356;
PRO4352; PRO4380; PRO4354; PRO4406; PRO4407; PRO4408

PRO4424; PRO4422; PRO4430; PRO4499; tumour; obesity; diabetes;

Schonlein-Henoch purpura; celiac disease; dermatitis herpetiformis; celiac disease

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FT	Modified-site	305..308	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	320..323	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	326..329	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	346..349	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	350..353	"N-glycosylation site"
FT		/note=	
FT	Modified-site	362..365	"N-glycosylation site"
FT		/note=	
FT	Modified-site	369..372	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	382..395	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	386..389	"casein kinase II phosphorylation site"
FT		/note=	
FT	Modified-site	387..390	"casein kinase II phosphorylation site"
FT		/note=	

XX WPI: 2000-628263/60.
DR N-PSDB; AAA96353.
XX
PT Novel secreted and transmembrane polypeptides useful for diagnosing
PT tumour in a mammal, for identifying agonists and antagonists of the
PT polypeptide and for therapeutic use
XX
PS Claim 12; Fig 36; 222pp; English.
XX
CC The present sequence represents a secreted or transmembrane polypeptide.
CC The specification describes polypeptides designated PRO1484, PRO4334,
CC PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4357, PRO4405,
CC PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5990,
CC PRO6030, PRO4424, PRO4423, PRO4430 and PRO4499. PRO1889 polypeptide is
CC useful for diagnosing tumour in a mammal. The polypeptides, their
CC agonists and antagonists are useful treating a condition associated with
CC expression or activity of the polypeptide. Conditions treated include
CC obesity, diabetes or hyper- or hypo-insulinemia. The polypeptides are
CC capable of inducing proliferation of mammalian kidney mesangial cells
CC and are therefore useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Bergers disease or other
CC nephropathies associated with Schonlein-Henoch purpura, celliac disease,
CC dermatitis herpetiformis or Crohns disease. The nucleic acids may be used
CC to generate transgenic animals for use in development and screening of
CC therapeutically useful reagents and also for chromosome identification
CC and tissue typing.
XX
SQ Sequence 468 AA;

Query Match 99.3%; Score 2384; DB 21; Length 468;
Best Local Similarity 99.1%; Pred. No. 2.3e-145;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWLVLVLPLOAFPPGSGQDKSLHNRELSAERPLNEOIAEAEEDKIKKTYPP 60
Db 1 MGFLGTGWLVLVLPLOAFPPGSGQDKSLHNRELSAERPLNEOIAEAEEDKIKKTYPP 60

QY 61 ENKPGQSNYSFVDNLNLLRAITEKEIEKERSIRSSPLDNKLNVEDVDSTKNRKLIDDY 120
Db 61 ENKPGQSNYSFVDNLNLLRAITEKEIEKERSIRSSPLDNKLNVEDVDSTKNRKLIDDY 120

QY 121 DSTKSGDLHKFODDPDGLHLDGTPLTAEEDIVHKTAARIYENDRAVEDKIVSKLLNLGL 180
Db 121 DSTKSGDLHKFODDPDGLHLDGTPLTAEEDIVHKTAARIYENDRAVEDKIVSKLLNLGL 180

QY 181 ITESQAHTLEDEVAEVLKLSKEANNYEEDPNKPTSTENOAGKIPEKVTMPAAIQDGL 240
Db 181 ITESQAHTLEDEVAEVLKLSKEANNYEEDPNKPTSTENOAGKIPEKVTMPAAIQDGL 240

QY 241 AKGENDETVSNLTLTNGLERTKTYSNDFRDFOYFPNFYALLKSIDSEKAEKETLI 300
Db 241 AKGENDETVSNLTLTNGLERTKTYSNDFRDFOYFPNFYALLKSIDSEKAEKETLI 300

QY 301 TIMKTLIDFVKMWVYGTISPEGVSYLENDEMIALQTKNKKLNATDNISKLPPAPSE 360
Db 301 TIMKTLIDFVKMWVYGTISPEGVSYLENDEMIALQTKNKKLNATDNISKLPPAPSE 360

QY 361 KSHEETSTKKEAAKWEKYSGLKDSKDDNSNPGKTDPEKGTAEVLEAIRKKNIEWLK 420
Db 361 KSHEETSTKKEAAKWEKYSGLKDSKDDNSNPGKTDPEKGTAEVLEAIRKKNIEWLK 420

QY 421 KHDKGNKEDYDLKMRDFINKQADAYVEKGLDKDEAEATKRIYSSL 468
Db 421 KHDKGNKEDYDLKMRDFINKQADAYVEKGLDKDEAEATKRIYSSL 468

RESULT 3
AAU12216
ID AAU12216 standard; Protein; 468 AA.
XX
AC AAU12216;
XX

DT 24-OCT-2001 (first entry)
XX
DE Human PRO5990 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO: mammalian; cancer; lung;
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
XX WO200140466-A2.
PN 07-JUN-2001.
PD
XX 01-DEC-2000; 2000WO-US32678.
XX
PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2001-408281/43.
DR N-PSDB; AAS21288.
XX
PT Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
PT lung, breast, prostate, cervical
XX
PS Claim 12; Fig 90; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or

CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 XX
 XX Sequence 468 AA;

Query Match 99.3%; Score 2384; DB 22; Length 468;
 Best Local Similarity 99.1%; Pred. No. 2.3e-145;
 Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWTWLVLPQAFPPKPGSQSKSLHNRLSAERPLNEQIAEAEDKIKKTYPP 60
 DB 1 MGFLGTGWTWLVLPQAFPPKPGSQSKSLHNRLSAERPLNEQIAEAEDKIKKTYPP 60
 QY 61 ENKPGQSNYSFVDNLLRAITEKEKIEKERSIRSSPLDNKLVNVEDVSTKNRKLIDDY 120
 DB 61 ENKPGQSNYSFVDNLLRAITEKEKIEKERSIRSSPLDNKLVNVEDVSTKNRKLIDDY 120
 QY 121 DSTKSGLDHKFQDDPDGLHOLDGTPLTAEIVHKAARIYEENDRAVDFKIVSKLLNLGL 180
 DB 121 DSTKSGLDHKFQDDPDGLHOLDGTPLTAEIVHKAARIYEENDRAVDFKIVSKLLNLGL 180
 QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTNMAAIODGL 240
 DB 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTNMAAIODGL 240
 QY 241 AKGENDETSTNLTTLNGLERRTKYSEDNPFQYFPNFPYALLKSIDSEKAEKETLI 300
 DB 241 AKGENDETSTNLTTLNGLERRTKYSEDNPFQYFPNFPYALLKSIDSEKAEKETLI 300
 QY 301 TIMKTLIDFVKMVKYGTISPGEVSVLENDEMIALQTKNLEKKNATDNISKLPAPSE 360
 DB 301 TIMKTLIDFVKMVKYGTISPGEVSVLENDEMIALQTKNLEKKNATDNISKLPAPSE 360
 QY 361 KSHEETDSTKEAAKMEYKGLSKDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIEWLK 420
 DB 361 KSHEETDSTKEAAKMEYKGLSKDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIEWLK 420
 QY 421 KHDKGNKEDYDLSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468
 DB 421 KHDKGNKEDYDLSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

RESULT 4
 AAB87600 standard; Protein; 468 AA.
 XX AAB87600;
 AC AAB87600;
 XX AAB87600;
 DT 15-MAY-2001 (first entry)
 XX Human PRO5990.
 DE Human; PRO protein; mapping.
 XX Human; PRO protein; mapping.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200116318-A2.
 XX WO200116318-A2.
 PD 08-MAR-2001.
 XX 08-MAR-2001.
 PF 24-AUG-2000; 2000WO-US23328.
 XX 24-AUG-2000; 2000WO-US23328.
 PR 01-SEP-1999; 99WO-US20111.
 PR 15-SEP-1999; 99WO-US21090.
 PR 07-DEC-1999; 99US-0169495.
 PR 09-DEC-1999; 99US-0170262.
 PR 11-JAN-2000; 2000US-0175481.

PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US0414.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 03-MAR-2000; 2000US-0187202.
 PR 25-APR-2000; 2000US-019397.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 05-JUN-2000; 2000US-0209832.
 XX (GETH) GENENTECH INC.
 XX
 XX Eaton DL, Fillvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI: 2001-183260/18.
 XX N-PSDB; AAF92132.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in
 PT molecular biology, including use as hybridization probes, and in
 PT chromosome and gene mapping.
 XX
 PS Claim 12: Fig 150; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping.
 XX
 SQ Sequence 468 AA;

Query Match 99.3%; Score 2384; DB 22; Length 468;
 Best Local Similarity 99.1%; Pred. No. 2.3e-145;
 Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWTWLVLPQAFPPKPGSQSKSLHNRLSAERPLNEQIAEAEDKIKKTYPP 60
 DB 1 MGFLGTGWTWLVLPQAFPPKPGSQSKSLHNRLSAERPLNEQIAEAEDKIKKTYPP 60
 QY 61 ENKPGQSNYSFVDNLLRAITEKEKIEKERSIRSSPLDNKLVNVEDVSTKNRKLIDDY 120
 DB 61 ENKPGQSNYSFVDNLLRAITEKEKIEKERSIRSSPLDNKLVNVEDVSTKNRKLIDDY 120
 QY 121 DSTKSGLDHKFQDDPDGLHOLDGTPLTAEIVHKAARIYEENDRAVDFKIVSKLLNLGL 180
 DB 121 DSTKSGLDHKFQDDPDGLHOLDGTPLTAEIVHKAARIYEENDRAVDFKIVSKLLNLGL 180
 QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTNMAAIODGL 240
 DB 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTNMAAIODGL 240
 QY 241 AKGENDETSTNLTTLNGLERRTKYSEDNPFQYFPNFPYALLKSIDSEKAEKETLI 300
 DB 241 AKGENDETSTNLTTLNGLERRTKYSEDNPFQYFPNFPYALLKSIDSEKAEKETLI 300
 QY 301 TIMKTLIDFVKMVKYGTISPGEVSVLENDEMIALQTKNLEKKNATDNISKLPAPSE 360
 DB 301 TIMKTLIDFVKMVKYGTISPGEVSVLENDEMIALQTKNLEKKNATDNISKLPAPSE 360
 QY 361 KSHEETDSTKEAAKMEYKGLSKDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIEWLK 420
 DB 361 KSHEETDSTKEAAKMEYKGLSKDSTKDDNSNPGGKTDEPKGTEAYLEAIRKNIEWLK 420
 QY 421 KHDKGNKEDYDLSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468
 DB 421 KHDKGNKEDYDLSKMRDFINKQADAYVEKGILDKEEAIAIKRIYSSL 468

RESULT 5
 ABG95925

Db 421 KHKKGKEDYDLSKMRDFINKQADAYVEKGILDKEAEAIKRIYSSL 468

RESULT 6

ABU69097
ID ABU69097 standard; Protein; 468 AA.

XX AC ABU69097;
XX DT 02-JUN-2003 (first entry)

XX DE Human PRO polypeptide #18.

XX KW Human; PRO polypeptide; secreted and transmembrane protein; cancer;
KW non-insulin dependent diabetes mellitus; septic shock; stroke;
KW rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;
KW psoriasis; inflammatory bowel disease; asthma; antidiabetic;
KW cytostatic; immunosuppressive; antineumatic; antiarthritic;
KW cerebroprotective; vasotropic; antipsoriatic; antiinflammatory;
KW antiasthmatic.

XX OS Homo sapiens.

XX PN US2003008348-A1.

XX PD 09-JAN-2003.

XX PF 26-DEC-2001; 2001US-0035855.

XX PR 14-MAY-1999; 99WO-US10733.
XX PR 02-DEC-1999; 99WO-US28551.

XX PR 22-DEC-1999; 99WO-US30720.
XX PR 01-MAR-2000; 2000WO-US05601.

XX PR 02-MAR-2000; 2000WO-US05841.
XX PR 22-MAY-2000; 2000WO-US14042.

XX PR 03-JUN-2000; 2000WO-US15264.
XX PR 23-AUG-2000; 2000WO-US23522.

XX PR 24-AUG-2000; 2000WO-US23328.
XX PR 01-DEC-2000; 2000WO-US32678.

XX PR 01-JUN-2001; 2001WO-US17800.
XX PR 20-JUN-2001; 2001WO-US19692.

XX PR 29-JUN-2001; 2001WO-US21066.
XX PR 05-JUL-2001; 2001WO-US21735.

XX PR 13-MAY-1998; 98US-085579P.
XX PR 15-DEC-1998; 98US-112514P.

XX PR 22-DEC-1998; 98US-113300P.
XX PR 23-DEC-1998; 98US-113430P.

XX PR 23-DEC-1998; 98US-113605P.
XX PR 22-JAN-1999; 99US-116843P.

XX PR 23-MAR-1999; 99US-125774P.
XX PR 23-MAR-1999; 99US-125778P.

XX PR 24-MAR-1999; 99US-125826P.
XX PR 31-MAR-1999; 99US-127035P.

XX PR 05-APR-1999; 99US-12706P.
XX PR 13-APR-1999; 99US-129122P.

XX PR 21-APR-1999; 99US-130359P.
XX PR 25-MAY-1999; 99US-135750P.

XX PR 08-JUN-1999; 99US-138166P.
XX PR 20-JUL-1999; 99US-144791P.

XX PR 03-AUG-1999; 99US-146970P.
XX PR 29-OCT-1999; 99US-162506P.

XX PR 16-AUG-2001; 2001US-0931836.

XX PA (GETH) GENENTECH INC.

XX PI Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
XX PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;

XX DR WPI; 2003-341326/32.
XX DR N-PSDB; ACA06116.

XX PT New PRO polypeptides and nucleic acid molecules, useful for diagnosing
or treating diabetes mellitus, cancers, septic shock, inflammatory

PT bowel disease or asthma, or in gene therapy, chromosome identification
XX or tissue typing
PS Claim 12; Fig 36; 196pp; English.

XX CC The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or
CC treating non-insulin dependent diabetes mellitus, cancers, septic
CC shock, rheumatoid arthritis, graft-versus-host disease, stroke, cardiac
CC ischaemia, psoriasis, inflammatory bowel disease or asthma. The PRO
CC polynucleotide sequences may be used as hybridisation probes in
CC chromosome and gene mapping, or in generating antisense RNA and DNA.
CC They are also useful in preparing PRO polypeptides, in assays to
CC identify other proteins or molecules involved in binding reaction, to
CC generate transgenic animals or knockout animals, which in turn are
CC useful in the development and screening of therapeutically useful
CC reagents, for chromosome identification, and tissue typing. The PRO
CC polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. Anti-PRO antibodies may be used in diagnostic assays for
CC PRO polypeptides, or for the affinity purification of the polypeptides
CC from recombinant cell culture or natural sources. ABU69080-ABU69102
CC represent the human PRO polypeptides of the invention.

XX SQ Sequence 468 AA;

Query Match 99.3%; Score 2384; DB 24; Length 468;
Best Local Similarity 99.1%; Pred. No. 2.3e-145;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGTLVLVLP IQAFPKPGSGDSKSLNRLSARPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGTLVLVLP IQAFPKPGSGDSKSLNRLSARPLNEQIAEAEEDKIKKTYPP 60

QY 61 ENKPGQSNYSFVDNLNLLRAITEKEKIERQSISSPLDNKLNVEDVDSTNRKLIDDY 120
DB 61 ENKPGQSNYSFVDNLNLLKAITEKEKIERQSISSPLDNKLNVEDVDSTNRKLIDDY 120

QY 121 DSTKSGLDHKKFQDDPDGLHQLDGTPLTAEDIVHKTAARIYEENDRAVDFKIVSKLLNLGL 180
DB 121 DSTKSGLDHKKFQDDPDGLHQLDGTPLTAEDIVHKTAARIYEENDRAVDFKIVSKLLNLGL 180

QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIDQGL 240
DB 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMAAIDQGL 240

QY 241 AKGENDETVSNTLTITNGLERTKTYSEDNFRDFQYFPNFIALLKSIDSEKAKEKETLI 300
DB 241 AKGENDETVSNTLTITNGLERTKTYSEDNFRDFQYFPNFIALLKSIDSEKAKEKETLI 300

QY 301 TIMKTLIDFVKMVKYGTISPPEGVSYLENLDEMIALQTKNKLKLNATONISKLFPPAPSE 360
DB 301 TIMKTLIDFVKMVKYGTISPPEGVSYLENLDEMIALQTKNKLKLNATONISKLFPPAPSE 360

QY 361 KSHETDSTKEEAAKMEKEYGSLKDSKDDNSNPGKTDPEPKGTEAYLEATRKNIWLK 420
DB 361 KSHETDSTKEEAAKMEKEYGSLKDSKDDNSNPGKTDPEPKGTEAYLEATRKNIWLK 420

QY 421 KHKKGKEDYDLSKMRDFINKQADAYVEKGILDKEAEAEAIKRIYSSL 468
DB 421 KHKKGKEDYDLSKMRDFINKQADAYVEKGILDKEAEAEAIKRIYSSL 468

RESULT 7

ABU69120

ID ABU69120 standard; Protein; 468 AA.

XX AC ABU69120;

XX DT 02-JUN-2003 (first entry)

XX

XX 01-MAY-2002; 2002US-0063512.
PF 06-DEC-2001; 2001US-0006867.
PR (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI: 2003-330984/31.
DR N-PSDB; ACA60437.
XX
XX New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to
PT the PRO polypeptide or antibody
XX
XX Disclosure: Fig 150; 409pp; English.
XX
XX The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
CC in assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This is the amino acid sequence of a novel
CC human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 468 AA;
Query Match 99.3%; Score 2384; DB 24; Length 468;
Best Local Similarity 99.1%; Pred. No. 2.3e-145;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGFLGTGWLVLVLPQAFKPGGSDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
Db 1 MGFLGTGWLVLVLPQAFKPGGSDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLLRAITEKEKIERQSISSPLDNKLNVEDVDSTKNRKLIDDY 120
Db 61 ENKPGQSNYSFVDNLNLLRAITEKEKIERQSISSPLDNKLNVEDVDSTKNRKLIDDY 120
QY 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIVHKTAARIYEENDRAVDFKIVSKLLNLGL 180
Db 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIVHKTAARIYEENDRAVDFKIVSKLLNLGL 180
QY 181 ITESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQDGL 240
Db 181 ITESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQDGL 240
QY 241 AKGENDETVSNLTLTNGLERRTKY SEDNPFDFQYFFNFYALLKSIDSEKAEKETLI 300
Db 241 AKGENDETVSNLTLTNGLERRTKY SEDNFEELYFPNFYALLKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFVKMMVYGTISP EEGVSYLENLDEM TALOTKKNLEKNATDNISKLPAPSE 360
Db 301 TIMKTLIDFVKMMVYGTISP EEGVSYLENLDEM TALOTKKNLEKNATDNISKLPAPSE 360
QY 361 KSHEETDSTKEAAKMEKEYSLKDS TKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLK 420
Db 361 KSHEETDSTKEAAKMEKEYSLKDS TKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGILDKEAEAIKRIYSSL 468
|||||

Db 421 KHKDKGNKEDYDLSKMRDFINKQADAYVEKGILDKEAEAIKRIYSSL 468
RESULT 10
ABU72183
ID ABU72183 standard; Protein; 468 AA.
XX
XX AC ABU72183;
XX DT 13-JUN-2003 (first entry)
XX DE Human PRO polypeptide #75.
XX KW Human; PRO polypeptide; secreted and transmembrane protein;
XX KW anti-PRO antibody; diagnostic assay; gene expression.
XX OS Homo sapiens.
XX US2003023042-A1.
XX PD 30-JAN-2003.
XX PF 01-MAY-2002; 2002US-0063502.
XX PR 06-DEC-2001; 2001US-0006867.
XX PA (GETH) GENENTECH INC.
XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX DR WPI: 2003-331484/31.
XX DR N-PSDB; ACA63447.
XX PT Novel monoclonal antibody that binds to secreted and transmembrane
XX polypeptide, useful for detecting and purifying the polypeptide and
XX also for treating conditions responsive to the antibody
XX
XX Disclosure: Fig 150; 408pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a
CC medicament useful in the treatment of a condition responsive to
CC anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic
CC assays for PRO, by detecting its expression in specific cells,
CC tissues or serum, and for affinity purification of PRO from
CC recombinant cell culture or natural sources. ABU72109-ABU72192
CC represent the human PRO polypeptides of the invention.
XX
SQ Sequence 468 AA;
Query Match 99.3%; Score 2384; DB 24; Length 468;
Best Local Similarity 99.1%; Pred. No. 2.3e-145;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MGFLGTGWLVLVLPQAFKPGGSDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
Db 1 MGFLGTGWLVLVLPQAFKPGGSDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLLRAITEKEKIERQSISSPLDNKLNVEDVDSTKNRKLIDDY 120
Db 61 ENKPGQSNYSFVDNLNLLRAITEKEKIERQSISSPLDNKLNVEDVDSTKNRKLIDDY 120
QY 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIVHKTAARIYEENDRAVDFKIVSKLLNLGL 180
Db 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIVHKTAARIYEENDRAVDFKIVSKLLNLGL 180
QY 181 ITESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQDGL 240
Db 181 ITESQAHTLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQDGL 240

DR WPI: 2003-332040/31.
XX N-PSDB; ACA03647.
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping; as chromosome markers, in
PT tissue typing, and in chromosome identification
XX
XX Claim 12; Fig 90; 660pp; English.
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for
CC linking bioactive molecules to cells expressing PRO polypeptides,
CC for modulating biological activities of cells expressing PRO
CC polypeptides, and for identifying agonists or antagonists.
CC The PRO polypeptides are useful for stimulating the release of
CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
CC the proliferation or differentiation of chondrocytes, and detecting the
CC presence of tumours. The polynucleotide sequences encoding PRO
CC polypeptides are useful as hybridisation probes, in chromosome and
CC gene mapping, in the generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptides, for generating transgenic animals or
CC knockout animals, for the genetic analysis of individuals with genetic
CC disorders, and in gene therapy. AB066570-AB066844 represent the human
CC PRO polypeptides of the invention.
CC Note: The sequence data for this patent was obtained in electronic
CC format directly from the USPTO web site at
CC seqdata.uspto.gov/psipdsidentry.html.
XX
XX Sequence 468 AA;
SQ

Query Match 99.3%; Score 2384; DB 24; Length 468;
Best Local Similarity 99.1%; Pred. No. 2,3e-145;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWILVLVLPQAFPPGGSQDKSLNRELNAERPLNEQIAEEDKIKKTYPP 60
DB 1 MGFLGTGWILVLVLPQAFPPGGSQDKSLNRELNAERPLNEQIAEEDKIKKTYPP 60
QY 61 ENKPGOSNYSFVDNLNLLRAITEKEKIEROSIRSSPLDNKLNVEDVDSTNKRLLIDDY 120
DB 61 ENKPGOSNYSFVDNLNLLRAITEKEKIEROSIRSSPLDNKLNVEDVDSTNKRLLIDDY 120
QY 121 DSTKSGLDHKFQDDPDLGHLQDGTPLTAEDIHVHKAARIYEENDRAVDFKIYSKLLNLGL 180
DB 121 DSTKSGLDHKFQDDPDLGHLQDGTPLTAEDIHVHKAARIYEENDRAVDFKIYSKLLNLGL 180
QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQDGL 240
DB 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTMPAAIQDGL 240
QY 241 AKGENDETNSVTLTNGLERTKYSEDNFDQYFPNFYALLKSIDSEKAKEKETLI 300
DB 241 AKGENDETNSVTLTNGLERTKYSEDNFDQYFPNFYALLKSIDSEKAKEKETLI 300
QY 301 TIMKTLIDPVMKMYGITSPEGVSYLENLDMALQTKNLEKATNIDNISKLPAPSE 360
DB 301 TIMKTLIDPVMKMYGITSPEGVSYLENLDMALQTKNLEKATNIDNISKLPAPSE 360
QY 361 KSHEETDSTKEEAARKEKEYGLSKDSTKDDNSNPGKTDPEPKGTEAYLEAIRKNIWLK 420
DB 361 KSHEETDSTKEEAARKEKEYGLSKDSTKDDNSNPGKTDPEPKGTEAYLEAIRKNIWLK 420
QY 421 KIDKKGKEDYDLSKMRDPINKQADAYVEKGLDKEEAIRKRIYSSL 468
DB 421 KIDKKGKEDYDLSKMRDPINKQADAYVEKGLDKEEAIRKRIYSSL 468

RESULT 12

AB066890

ID AB066890 standard; Protein; 468 AA.

XX

AC AB066890;
XX
XX 27-MAY-2003 (first entry)
DE Human secreted/transmembrane, PRO, protein SEQ ID 90.
XX
KW Human; secreted protein; transmembrane protein; PRO;
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
KW infertility; birth defects; premature aging; AIDS; biosensor;
KW acquired immunodeficiency syndrome; cancer; diabetic complication;
KW bioreactor; tumour.
XX
OS Homo sapiens.
XX US2003032155-A1.
XX
XX 13-FEB-2003.
XX
XX 03-MAY-2002; 2002US-0137865.
XX
XX 31-MAR-1997; 97WO-US05230.
XX 12-JUN-1998; 98WO-US12456.
XX 14-JUL-1998; 98WO-US14552.
XX 28-AUG-1998; 98WO-US17888.
XX 10-SEP-1998; 98WO-US18824.
XX 14-SEP-1998; 98WO-US19093.
XX 14-SEP-1998; 98WO-US19094.
XX 14-SEP-1998; 98WO-US19177.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 29-OCT-1998; 98WO-US22991.
XX 20-NOV-1998; 98WO-US24855.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 10-MAR-1999; 99WO-US05190.
XX 20-APR-1999; 99WO-US08615.
XX 14-MAY-1999; 99WO-US10733.
XX 02-JUN-1999; 99WO-US12252.
XX 01-SEP-1999; 99WO-US20111.
XX 08-SEP-1999; 99WO-US20594.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 05-OCT-1999; 99WO-US23089.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28313.
XX 30-NOV-1999; 99WO-US28409.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 02-DEC-1999; 99WO-US28551.
XX 02-DEC-1999; 99WO-US28564.
XX 02-DEC-1999; 99WO-US28565.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 20-DEC-1999; 99WO-US30999.
XX 22-DEC-1999; 99WO-US30720.
XX 30-DEC-1999; 99WO-US31243.
XX 30-DEC-1999; 99WO-US31274.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00277.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 18-FEB-2000; 2000WO-US04342.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 01-MAR-2000; 2000WO-US05601.
XX 02-MAR-2000; 2000WO-US05746.
XX 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21738.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-APR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866038.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 PR (GETH) GENENTECH INC.

XX Baker KP, Beresini M, DeForge L, Desnoyers L, Fillvaroff E, Gao W;
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX WPI: 2003-331925/31.
 DR N-PSDB: ACA04068.

XX New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 XX Claim 12; Fig 90; 659pp; English.
 XX The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of

CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC or the differentiation of adipocyte cells, a method for factor VITA,
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.

XX SQ Sequence 468 AA;

Query Match 99.3%; Score 2384; DB 24; Length 468;
 Best Local Similarity 99.1%; Pred. No. 2.3e-145;
 Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGTWLVLPVLPQAPKPGSQDKSLHNRELSAERPLNEQIAEEDKIKKTYPP 60
 DB 1 MGFLGTGTWLVLPVLPQAPKPGSQDKSLHNRELSAERPLNEQIAEEDKIKKTYPP 60
 QY 61 ENKPGOSNYSFVDNLLRAITEKIEKERSQSRSPDLNKLNVEDVDSTKNRKLIDDY 120
 DB 61 ENKPGOSNYSFVDNLLRAITEKIEKERSQSRSPDLNKLNVEDVDSTKNRKLIDDY 120
 QY 121 DSTKSLDHLKFDQDDPDLHQLDGTPLTAEDIVHKIAARIYEENDRAVDFKIYVKLLNLGL 180
 DB 121 DSTKSLDHLKFDQDDPDLHQLDGTPLTAEDIVHKIAARIYEENDRAVDFKIYVKLLNLGL 180
 QY 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENAGKIPKVTMAATQDGL 240
 DB 181 ITESQAHTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENAGKIPKVTMAATQDGL 240
 QY 241 AKGENDETYSNTLTITNGLERRTKTYSNDFDFQVFPNFFYALLKSIDSEKAKKETLI 300
 DB 241 AKGENDETYSNTLTITNGLERRTKTYSNDFDFQVFPNFFYALLKSIDSEKAKKETLI 300
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 DB 301 TIMKTLIDFVKMWKYGTISPPEGVSYLENDEMIALQTKNKLKNATDNISKLPAPSE 360
 QY 361 KSHEETDSTKEEAAKMEKYEYGLSKDSTKDDNSNPGGKTDEPKGKTEAVLEAIRKNIEWLK 420
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 DB 421 KDKKGNKEDYDLNKLKRDYFINKQADAYVEKGLDKEEAEAIKRIYSSL 468

RESULT 13

ABU59695
 ID ABU59695 standard; Protein; 468 AA.
 AC ABU59695;
 XX ABU59695;

DT 13-MAY-2003 (first entry)
 XX 13-MAY-2003 (first entry)
 DE Novel secreted and transmembrane protein PRO5990.

XX Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-Fos induction;

vascular endothelial growth factor inhibition; VEGF inhibition;
 endothelial cell growth inhibitor; T-lymphocytes stimulation;
 retinal neurons cell survival; rod photoreceptor cell survival;
 retinal disorder; retinitis pigmentosa; kidney disorder;
 mammalian kidney mesangial cell proliferation; Berger disease;
 dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 chondrocyte redifferentiation; sports injury; arthritis.

Homo sapiens.

US2003017563-A1.

23-JAN-2003.

07-MAY-2002; 2002US-0140808.

31-MAR-1997; 97WO-US05230.

12-JUN-1998; 98WO-US12456.

14-JUL-1998; 98WO-US14552.

28-AUG-1998; 98WO-US17888.

10-SEP-1998; 98WO-US18824.

14-SEP-1998; 98WO-US19093.

14-SEP-1998; 98WO-US19094.

14-SEP-1998; 98WO-US19177.

16-SEP-1998; 98WO-US19330.

17-SEP-1998; 98WO-US19437.

07-OCT-1998; 98WO-US21141.

29-OCT-1998; 98WO-US22991.

29-OCT-1998; 98WO-US22992.

20-NOV-1998; 98WO-US24855.

01-DEC-1998; 98WO-US25108.

05-JAN-1999; 99WO-US00106.

08-MAR-1999; 99WO-US05028.

10-MAR-1999; 99WO-US05190.

20-APR-1999; 99WO-US08615.

14-MAY-1999; 99WO-US10733.

02-JUN-1999; 99WO-US12252.

01-SEP-1999; 99WO-US20111.

08-SEP-1999; 99WO-US20594.

13-SEP-1999; 99WO-US20944.

15-SEP-1999; 99WO-US21090.

15-SEP-1999; 99WO-US21547.

05-OCT-1999; 99WO-US23089.

29-NOV-1999; 99WO-US28214.

30-NOV-1999; 99WO-US28313.

30-NOV-1999; 99WO-US28409.

01-DEC-1999; 99WO-US28301.

01-DEC-1999; 99WO-US28634.

PR 30-MAR-2000; 2000WO-US08439.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US20710.

PR 11-AUG-2000; 2000WO-US22031.

PR 23-AUG-2000; 2000WO-US23222.

PR 24-AUG-2000; 2000WO-US23328.

PR 08-NOV-2000; 2000WO-US30952.

PR 10-NOV-2000; 2000WO-US30873.

PR 01-DEC-2000; 2000WO-US32678.

PR 20-DEC-2000; 2000WO-US34956.

PR 28-FEB-2001; 2001WO-US06520.

PR 01-MAR-2001; 2001WO-US06666.

PR 25-MAY-2001; 2001WO-US17092.

PR 01-JUN-2001; 2001WO-US17800.

PR 20-JUN-2001; 2001WO-US19692.

PR 22-JUN-2001; 2001WO-US20116.

PR 29-JUN-2001; 2001WO-US21066.

PR 09-JUL-2001; 2001WO-US21735.

PR 20-DEC-2000; 2000US-0747259.

PR 28-FEB-2001; 2001US-0796498.

PR 09-MAR-2001; 2001US-0802706.

PR 14-MAR-2001; 2001US-0808689.

PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.

PR 25-MAY-2001; 2001US-0866028.

PR 18-MAY-2001; 2001US-0854280.

PR 10-MAY-2001; 2001US-0854208.

PR 01-JUN-2001; 2001US-0872035.

PR 05-JUN-2001; 2001US-0874503.

PR 14-JUN-2001; 2001US-0882636.

PR 19-JUN-2001; 2001US-0886342.

PR 21-JUN-2001; 2001US-0887879.

PR 18-JUL-2001; 2001US-0908827.

PR 06-AUG-2001; 2001US-0924419.

PR 09-AUG-2001; 2001US-0927796.

PR 16-AUG-2001; 2001US-0931836.

PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;

WPI; 2003-148238/14.

N-PSDB; ABX89185.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346

and PRO1375, which stimulate proliferation of stimulated T-lymphocytes

are therapeutically useful for enhancing immune response and in cancer

treatments

Claim 12; Fig 90; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO

polypeptides are useful in detecting PRO polypeptides in a sample, in

linking a bioactive molecule to a cell expressing a PRO polypeptide, and

in modulating at least one biological activity of a cell expressing a PRO

polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus

useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186

stimulate adrenal cortical capillary endothelial growth, and PRO536,

PRO943, PRO828, PRO1068 or PRO826, PRO826, PRO819, PRO1126,

PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus

useful for treating conditions or disorders where angiogenesis would be

beneficial, e.g. wound healing and antagonism of this polypeptide are

useful for treating cancerous tumours. PRO812 inhibits vascular

endothelial growth factor (VEGF) stimulated proliferation of endothelial

cells and is thus useful for inhibiting endothelial cell growth in

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 10:19:48 ; Search time 42 Seconds
(without alignments)
471.464 Million cell updates/sec

Title: US-09-554-945B-2
Perfect score: 2402
Sequence: 1 MGFLGTGTLVLVLPQAF.....EKGILDKREAEAIRIYSSL 468

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	173	7.2	1786	3 US-08-973-462-8	Sequence 8, Appli
2	169.5	7.1	1164	3 US-08-923-992A-2	Sequence 2, Appli
3	169	7.0	1098	3 US-08-923-992A-8	Sequence 8, Appli
4	168	7.0	1164	3 US-08-923-992A-10	Sequence 10, Appli
5	166	6.9	1128	3 US-08-923-992A-6	Sequence 6, Appli
6	165	6.9	1104	3 US-08-923-992A-4	Sequence 4, Appli
7	162.5	6.8	957	4 US-09-914-259-16	Sequence 16, Appli
8	162	6.7	2662	4 US-09-595-684B-31	Sequence 31, Appli
9	158.5	6.6	816	2 US-08-533-306A-6	Sequence 6, Appli
10	158.5	6.6	816	2 US-08-742-923A-6	Sequence 6, Appli
11	158.5	6.6	956	4 US-09-914-259-17	Sequence 17, Appli
12	158	6.6	2285	4 US-09-308-375-2	Sequence 2, Appli
13	157.5	6.6	885	2 US-08-533-306A-4	Sequence 4, Appli
14	157.5	6.6	885	2 US-08-742-923A-4	Sequence 4, Appli
15	155	6.5	1354	3 US-08-685-871-2	Sequence 2, Appli
16	155	6.5	8991	4 US-08-714-741-32	Sequence 32, Appli
17	153.5	6.4	984	1 US-08-242-932-2	Sequence 2, Appli
18	153.5	6.4	984	1 US-08-714-481-2	Sequence 2, Appli
19	153.5	6.4	984	5 PCT-US95-06111-2	Sequence 2, Appli
20	149	6.2	1588	5 PCT-US93-07261-11	Sequence 11, Appli
21	149	6.2	1663	5 PCT-US93-07261-16	Sequence 16, Appli
22	147.5	6.1	1087	4 US-09-914-259-12	Sequence 12, Appli
23	147.5	6.1	1231	4 US-08-714-741-41	Sequence 41, Appli
24	147	6.1	588	4 US-08-714-741-42	Sequence 42, Appli
25	145.5	6.1	864	4 US-08-714-741-40	Sequence 40, Appli
26	145	6.0	534	4 US-09-103-664A-2	Sequence 2, Appli
27	145	6.0	3111	2 US-08-460-309-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-973-462-8

; Sequence 8, Application US/08973462B

; Patent No. 6191270

; GENERAL INFORMATION:

; APPLICANT: DRUILHE, PIERRE

; APPLICANT: DAUBERSIES, PIERRE

; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES

; FILE REFERENCE: 0660-0125-0 PCT

; CURRENT APPLICATION NUMBER: US/08/973,462B

; CURRENT FILING DATE: 1998-02-06

; EARLIER APPLICATION NUMBER: PCT/FR96/00894

; EARLIER FILING DATE: 1996-06-12

; EARLIER APPLICATION NUMBER: FR 95/07007

; EARLIER FILING DATE: 1995-06-13

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 1786

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide

US-08-973-462-8

Query Match	7.2%	Score 173;	DB 3;	Length 1786;
Best Local Similarity	22.0%	Pred. No. 0.00029;		
Matches 120;	Conservative 91;	Mismatches 204;	Indels 130;	Gaps 26;
QY	27	QDKSLHRELAE--RPLNEQIAEAEEDKIKKTPPENKPGQSN-----YSFVDNL--	75	
Db	957	ENAVESNENVAENAEKLNKLVNTVLDKVEETVETSGESLENEMDKRAFFSEIFDNVKG	1016	
QY	76	---NLLR-----AITEKEKEKERQSRSSPLDNKLN-----VEDVDSTK--	112	
Db	1017	IQENLLTGMRFSIETSIIVQSEKVDL-NENVSILONIKMKGLLNKLENISTEGV	1075	
QY	113	-----NRKLDDYD-----STKSGLDHKFDQDDGLHOLDGPLTAEDI-	151	
Db	1076	QETVTEHVQNVYVDVPMKKDQFLGILNEAGGKEMFFNLED-VFSESVDIVVEEK	1134	
QY	152	-----VHKIAARTYENDRAVDFKIVSKLLNLGLITTESQAHTLEDEVAEVLQKLI----	201	
Db	1135	DEPVQKEVEKETVSIIEEENIVD-----VLEEKEDLTKMIDAVEESIETS	1183	
QY	202	--SKANNYEEDPNKPTSWT-----ENQAGKIPKVTPTMAATQDGLAKE---NDETYSN	251	
Db	1184	SDSKETESIKDKEDVSLVVEEQDNDMDDESVEKVLKLNMEELMKDAVEIND-----	1238	
QY	252	TITLTNGLRRRTKTYSE---DNFRDQYFPFNALLKS-----IDSEKEAKEK--ETLIT	301	

Db 1239 ---INSLIETQELNEVADLIKONEKMLEKALSDESKSDEIDAKDDTLEKVEEHD 1295
 QY 302 IMKTLIDFVMM-VKYGISPEEGVSYLENDEMIALQTK--NKLEKNATONISKLPAP 358
 Db 1296 ITTLDVEVELKDVDEEKI---EKVSDLKLEEDILKEVKEKELESEILEDEYKELKTIE 1352
 QY 359 SKSSEHEEDTSKEAAKMEKEVGLSKDSTKDDNSNPGKTDPEPKGTAYLEAIRKNIEW 418
 Db 1353 TDILEEKEIEKHDFEKEFEAEETKDLFADILAEVSSLEVEEKKLEBEVHE-LKEEVEH 1411
 QY 419 LKKHDK--KGNKEDYDLKMRDFFINKOADAY---VEKGILDK-----FEARAK 462
 Db 1412 IISGDAHLKGLEED-DLEEVDDLKGSILMLKGMELGDMDKESLEDVTTKLGERVESLK 1470
 QY 463 RIYSS 467
 Db 1471 DVLSS 1475

RESULT 2

US-08-923-992A-2
 ; Sequence 2, Application US/08923992A
 ; Patent No. 6280738

GENERAL INFORMATION:

APPLICANT: Tai, Joseph Y.
 APPLICANT: Blake, Milan S.
 TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B
 TITLE OF INVENTION: Streptococcal Beta Antigens
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/923,992A
 FILING DATE: 05-SEP-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/024,707

FILING DATE: 06-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1438.0140001/RWE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1164 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-923-992A-2

Query Match 7.1%; Score 169.5; DB 3; Length 1164;

Best Local Similarity 21.4%; Pred.No. 0.0003;

Matches 123; Conservative 78; Mismatches 189; Indels 185; Gaps 25;

QY 36 LSAERPLNE-----QIAEAEDEKIKKTYPPENKPGQSNYSFVDNLLNLRAT-EKEK 86

Db 149 LELENQFNETNRLHLIKQHEEVEKDKAK-----QKTLKQSDTKVDLSNIDKELNHQSQ 204

QY 87 IEK--ERQSIRSPDLNKL-----NVEDVDSTKNRKLIDDYDSTKSGLDHK 130

Db 205 VEKMAEQKITNEDKDSMLKKIEDIRKQAQADKKDEAEVKVREELKGLFSTTRAGLDQE 264
 QY 131 FQDDPDGLHQLDGLPLTAEDIVHKI-----AARIYEENDRAVEDKIVSKLNLG 179
 Db 265 IQE-----HVKKET--SEENTQKVDHYANSLQNLAKQSLSELDKATTNEQATQVKNQF 317
 QY 180 L-----ITESQAHLEDEVAEV-----LQKLISKE--ANNYEE 210
 Db 318 LENAQKLEKETOPLIKETNVKLYKAMSELSQVEKELKHNSANLEDLVAKSKEIVREYEG 377
 QY 211 DPNKPTSWTE-----NOAGKPIPEKVTMPMAAIOGLAKGENDETYSN 251
 Db 378 KLQSKNLPKLQLEEAHSHKLQVVEDFRKKFKTSQVTPKKRVKRDLAANENQ--Q 434
 QY 252 TLTLTNGLERTKTYSEDNFRDQYFPNFYALKLSIDSEKAEKETLITIMKTLIDFVK 311
 Db 435 KIELTVSPENITVVEGED-----VKFTVTAKS-DS-----KTLDFSD 471
 QY 312 MMVKG-TISPEEGVSYLENLD-----EMIALQTK-----NKLEKNATD 349
 Db 472 LLTKYNPSVSDRISTNVKNTNDNHKTAETIKNLKLNESQTVILKAKDDSGNVVEKFTTI 531
 QY 350 NISKLFPAPSEKSHEETDSTKEAA-----KMEKEYGS LKD 385
 Db 532 TVQKKEEKQVPTPEQKDSKTEEKVQEPKSNKQNLQELIKSAQOELEKLEKAIKELME 591
 QY 386 STKDDNSNPGKTDPEKGTAEVLAIRKNIEWLKK-----HDKKGKEDYDLKSKMRDIN 441
 Db 592 Q-PEIPSNP--EYGIQKSIWESQKEPIQEAITSFKKIIGDSSSKYYTEHYFNKYKSDFMN 648
 QY 442 KQADAYVEKGILDKKEAE-----AIKRIYSS 467
 Db 649 YQLHAQME--MLTRKVQVMNKPYNDAEIKKIFES 681

RESULT 3

US-08-923-992A-8

; Sequence 8, Application US/08923992A

; Patent No. 6280738

GENERAL INFORMATION:

APPLICANT: Tai, Joseph Y.

APPLICANT: Blake, Milan S.

TITLE OF INVENTION: No. 6280738-IgA Fc Binding Forms of the Group B

TITLE OF INVENTION: Streptococcal Beta Antigens

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/923,992A

FILING DATE: 05-SEP-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/024,707

FILING DATE: 06-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1438.0140001/RWE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 8:

Db 194 KIEDIRKQAQADKEDAEVKBREELKLFSSKTRAGLDQQIQE-----HVKKET--SSEE 246
QY 151 IVHKI-----AARIYEENDRAVDFKIVSKLLNLGL----- 180
Db 247 NTQKVDEHYANSLQNAKSLSELDKAPTNEQATOVKNQFLENQAKLKEIQLIKETNVK 306
QY 181 ITESQAHTLEDAEAEV-----LQKLISKE---ANNYEEDPNKPTSWTE----- 220
Db 307 LYKAMESLEQVEKELKINSEANLQDLVAKSKEIVREYEGKLNQSKNPELKQLEEEAHS 366
QY 221 -----NOAGKIPKVTMAAIOGLAKGENDETVSNLTITLNGLERRTKYSEDNF 271
Db 367 KIKQVVEHFKKFTSEQVTPKRVKRDLANENNQ-----QKIELTVSPENITVYEGED-- 421
QY 272 RQDFQFPNFPYALLSIDSEKAKEKETLITIMKTLDIVKMMVKY--TISPEEGVSYLEN 330
Db 422 -----VKFTVTAKS-DS-----KTLDFSDLLTKYNSVSDRISTNYKTN 460
QY 331 LD-----EMIALQTK-----NKLEKNATDNI-----SKLFPAPSEKSHEE 365
Db 461 TDNHKIAELITIKNLKNSQVITLAKDDSGNVVEKTTITVQKKEEKQVKTPEQKHKS 520
QY 366 TD-----STKEAAKMEKEYGSLKDKSTKDDNSNP---GGKTDEPKG 403
Db 521 TEQNVPOEPKSNKQNLQELIKSAQOELEKLEKAIKELMEQ-PEIPSPNPEYGIQKSIWES 579
QY 404 KTEAYLEAIRKNIEWLKHDKKNGKEDYDLKMRDFINKQADAYVEKGILKEAE----- 459
Db 580 OKEPTQEAITSFNKITIGDSSSKYTYEHFNKYKSHFMNYQLHAQME--ILTRKVVQYMNK 637
QY 460 -----AKRIYSS 467
Db 638 YPDNAEIRKIPES 650

RESULT 7

US-09-914-259-16
; Sequence 16, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-914-259-16

Query Match 6.8%; Score 162.5; DB 4; Length 957;
Best Local Similarity 19.8%; Pred. No. 0.00075;
Matches 102; Conservative 96; Mismatches 179; Indels 137; Gaps 23;

QY 25 GSQDKSLHNR-----ELSAERPLNEQIAEAEEDKIKTYPPENKPGQSNYSFVDNLNLL- 78
Db 321 GORAKTIRKTVSNLELTAE-----ENKKYKEKEKKNKTLKNVIOHLEWEL 367

QY 79 -----RAITEKEKEKQSRSSPLDNKLNVEDVD-----STKNRKLIDDYDSTKSG 126
Db 368 NWRNGEAVPEQISAKDQK-NLEPCDNTPIIDNAPVWAGISTEEK---EKYDEEISS 423
QY 127 LDHKFQDDPDGHLQDGTPLFADIVHKAARIYEEND-----RAVDFKIVSKLLNLGLI 181
Db 424 LYRQLDDKDDQNEQ-----OSOLAELKQOQMLDQDELLASTRRDYERKIQBELRLQTE 476
QY 182 TESQAHTLEDAEAEVLOKLISKEANNYE---EDPNKPTSWTENQAGKIPEKVTMAAIOQ 238

Db 477 NEA-----AKDEVKEVLQAL-BELAVNYDOKSOEVEDKTRANEQLTDELAQKTTTLTTTQR 531
QY 239 GLAK-----GENDETYSNTLTLNGLERRTKTYSE 268
Db 532 ELSQLOEVSNHQKRRATEILNLLKDLGEIGIIGTND---VKTLDVNGVIEEFTWAR 588
QY 269 DNFRDQFPNFPYALLKSI-----DSEKEAKEKETLITIMKTLDIVKMMVKY 316
Db 589 -----LYISKMSKSEKSVLNRSKQLESAQMDSNRKMNASERELAACOLLISQHEAKIKS 642
QY 317 GTISPEEGVSYLENDEMIALQTKNKKLEK---NATDNISKLPAPSEKSHEDTSTKE-- 371
Db 643 LT-----DYMQNM-----QKRQLEESQDSISELAKL---RAQEKMHVEVSFQDKEKE 688
QY 372 -----EAAKMEKEYGSLKDKSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKHDKK 425
Db 689 HLTRQDAEMKKALEQQMHREAHQKLSRLDEIBEKOKIIDEIRDLNOKLOLEQEK 748
QY 426 GNKEDYDLKMRDFINKQADAYVEKGIL--DKEE 457
Db 749 -LSSDYNKLIKIED---QEREMKLEKLLLLNDKRE 778

RESULT 8

US-09-595-684B-31
; Sequence 31, Application US/09595684B
; Patent No. 6544766
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Ohashi, Cara
; APPLICANT: Sakowicz, Roman
; APPLICANT: Vaisberg, Eugeni
; APPLICANT: Wood, Kenneth
; APPLICANT: Yu, Ming
; TITLE OF INVENTION: Human kinesins and methods of producing
; and purifying human kinesins
; FILE REFERENCE: CYtop036
; CURRENT APPLICATION NUMBER: US/09/595,684B
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2662
; TYPE: PRT
; ORGANISM: Human
US-09-595-684B-31

Query Match 6.7%; Score 162; DB 4; Length 2662;

Best Local Similarity 21.6%; Pred. No. 0.0033;
Matches 118; Conservative 103; Mismatches 176; Indels 150; Gaps 28;

QY 26 SODKSLHNRRELSAERPLN---EQIAEAEEDKIKTYPPENKPGQSNYSFVDNLNLRAT 82
Db 1101 AOEK---NHAIKKEGELSRTCDRLAEVEEKEKESQLOEQQL-----LNQOEEMS 1150
QY 83 EKEKEKEKQSRSSPLDNKLNVEDVDSTK---NRKLIDDYDSTKS-----GLDHHK 130
Db 1151 EMQKINETENLKNELKNKELTLEHMETERLELAQKLNENYEEVKSIKERKVKLELOKS 1210
QY 131 FODDDPGL---HQLDGTPL-TAEDI---VH-KIAARIYEENDRAVDFKIVSKLLNLGL 180
Db 1211 FETERDHLRGYIREIATEGLQTKELKIAHILHKEHQETIDELRVSSEK-TAQIINTQD 1269
QY 181 ITESQAHTLEDAEAEVL---QKLIS---KEANNYEEDPNKPTSWTENQAGKIPEKVTMAA 235
Db 1270 LEKS--HTKLOEIPVLHHEEQELLPNKKVSETQETMNELELLTEOSTTK---DSTTLAR 1324
QY 236 IQ-----DGLAK-GENDETYSNTL-----TLNGLERRTK 264
Db 1325 IEMERLRLNEKFSQEEIKSLTKERDNLKTIKEALEVKHDLKHEIRETLAKIQSSQSK 1384

QY 265 TYSDFPRD-----FQYFNPYALK-----SIDSEKE-AKEKE 297
 Db 1385 QEQSLNKKEDNETTKIVSEMEQPKDSALLRIEIMGLSKRLQSDHDMKSVAKED 1444
 QY 298 TLITIMKTLDIFVKMVKYGTISPGEVSVYLENDEMIA--LOTNKNLE-----KNATD 349
 Db 1445 DLQRLQEV-----QSESDQLENKEIYAKHLETEEBELKVAHCCCKRQEE 1490
 QY 350 NISLFPAPSKSHEETDSTKEEAAKMEKEYGSLKSTKDDNSNPGGKTDEPKKTE--- 406
 Db 1491 TINELRVNLSEK-----ETEISTIQKLEANDKLN-----KIQEIYEKEEQLN 1535
 QY 407 -AYLEARKNIWELKHKDKGNKEDYD-----SKMRDFINQADAYVEKGLDKEEAEAI 461
 Db 1536 IKQISEVOENVNLKQPKHKKAKDSALQSTESKMLELTNRLOBSQEIQIMIKEK-EEM 1594
 QY 462 KRIYSSL 468
 Db 1595 KRQVEAL 1601

RESULT 9

US-08-533-306A-6

; Sequence 6, Application US/08533306A

; Patent No. 5837457

; GENERAL INFORMATION:

; APPLICANT: Liu, Pu

; APPLICANT: Collins, Francis S.

; APPLICANT: Siciliano, Michael J.

; APPLICANT: Claxton, David

; TITLE OF INVENTION: Markers for Detection of Chromosome 16

; TITLE OF INVENTION: Rearrangements

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.

; STREET: P.O. Box 828

; CITY: Bloomfield Hills

; STATE: MI

; COUNTRY: USA

; ZIP: 48303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/533,306A

; FILING DATE: September 25, 1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Deann F.

; REGISTRATION NUMBER: 36683

; REFERENCE/DOCKET NUMBER: 2115-00869COB

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (810) 641-1600

; TELEFAX: (810) 641-0270

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 816 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-533-306A-6

Query Match

Best Local Similarity 22.6%; Pred. No. 0.0012;

Matches 110; Conservative 82; Mismatches 186; Indels 109; Gaps 22;

QY 26 SODKSLHNELSRLNQCIAEEDKTKKYPNPKGQSNYSV--DNINLRAITE 83

Db 158 SHREEMENEVSVTGMLNE--AEGKAIKLAKDVASLSQLOQTQELLQEBETROKLVSK 215

QY 84 KEKIERQSR---SSPLDNKLNVEDVDSTKN-----RKLDDYDSTKSLGDH---KF 131

Db 216 LRQLEERNLSIQDQDDEEMAKQNLERHISTNLQLSKSKKLQDFASTVEALEEGKKRF 275
 QY 132 QDDPDGLHOLDGPTLTAEDIVHKIAARIYEENDRAVED-----KIVSKLLNLGLITISQA 186
 Db 276 QKEIENITQOYEEKAAAYDKLETKNRLQOQELDDLVVVDLQNRQLVSNL-----EKKQ 328
 QY 187 HTLEDEVAEVLQKLISKEANNYEDPNKPTSWTENQAGKIPEKVTPTMA-AIQDGL-AKGE 244
 Db 329 RKFOLLAE--EKNI--SKYADDER--AAEAAREKETKALSARALEEAEAKEE 379
 QY 245 NDETVSNLTLTNGLERRTKTYSDNFRDFQYFPNFYALKSIDSDS-----EKEAKEK 296
 Db 380 LERT-----NKLKAEMED-----LVSSKDDVGVKNVHELEKSKRAL 415
 QY 297 ETLITIMKTLDIFVKMVKYGTISPGEVSVYLENDEMIALQTKNKLKKNATONISK--- 353
 Db 416 ETQMEEMKTQLEEEDELQ-----ASEDAKLRLVNMQALKGQFERDLQARDEQNEEKRRQ 471
 QY 354 ----LFPAPSEKSHEETDSTKEEAAKMEKEYGSLKSTKDDNSNPGGKTDEPK--GKTEA 407
 Db 472 LQRLHEYTELEDERNERALAAAAKKLE-GDLKDLQADSAIKGREAIIQLRLQA 530
 QY 408 YLEAIRKNIE-----WLKHKDKGNKEDYDLSKMRDFI-----NKQADAYVEK 450
 Db 531 QMRDQFQLEADARASDEIFATAKENEKAKSLEADLMQLEDLAAAEARAKQAD----- 585
 QY 451 GILDKEE 457
 Db 586 --LEKEE 590

RESULT 10

US-08-742-923A-6

; Sequence 6, Application US/08742923A

; Patent No. 5869611

; GENERAL INFORMATION:

; APPLICANT: Liu, Pu

; APPLICANT: Collins, Francis S.

; APPLICANT: Siciliano, Michael J.

; APPLICANT: Claxton, David

; TITLE OF INVENTION: Markers for Detection of Chromosome 16

; TITLE OF INVENTION: Rearrangements

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.

; STREET: P.O. Box 828

; CITY: Bloomfield Hills

; STATE: MI

; COUNTRY: USA

; ZIP: 48303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/742,923A

; FILING DATE: No. 5869611ember 1, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Deann F.

; REGISTRATION NUMBER: 36683

; REFERENCE/DOCKET NUMBER: 2115-00869DVC

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (810) 641-1600

; TELEFAX: (810) 641-0270

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 816 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-742-923A-6

Query Match 6.6%; Score 158.5; DB 2; Length 816;
Best Local Similarity 22.6%; Pred. No. 0.0012;
Matches 110; Conservative 82; Mismatches 186; Indels 109; Gaps 22;

QY 26 SODKSLNRELISAERPLNEQIAEAEDKIKKTYPPENKPGOSNYSFV--DNLNLLRAITE 83
DB 158 SHREMEENEVSVTGMLNE--AEGKAIKLAKDVAASLSOLODTELLOEETROKLVSTK 215
QY 84 KEKTEKQSTR-----SSPLDNKLNVEDVDSTKN-----RKLIDDYDSTKGLDH---KF 131
DB 216 LRQLEERNLSQDQDDEMEAKQNLERHISTNLQSDSKKKLQDFASTVEALEEGKKRF 275
QY 132 QDDPDGLHOLDGTPLTAEIDIVHKIAARIYENDRAVFD-----KIVSKLLNGLITESQA 186
DB 276 QKEIENLTQQYEKAAAYDKLETKNRLQOELDLVVDLQNRQLVSNL-----EKKQ 328
QY 187 HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMA-AIQDGL-ARKE 244
DB 329 RKFDQLAE--EKNIS---SKYADEROR---AEAEAREKETKALSARALEALEAKEE 379
QY 245 NDETVSNLTLTNGLERRTKTYSEDNFRDFOYFNFVALLKSID-----EKEAKEK 296
DB 380 LERT-----NKLKAEEMED-----LVSSKDDVGKNVHELEKSKRAL 415
QY 297 ETLITIMKTLIDFVKMVKYGTISPESGVSYLENLDEMIALQTKNLEKNATDNISK--- 353
DB 416 ETQMEEMKTOLEEELELQ-----ASEDAKLEVNMQALKGOFERDLOARDEQNEEKRRQ 471
QY 354 ---LFPAPSEKSEETDSTKEAAKMEKEGSLKSTKDDNSNPGGKTDEPK--GKTEA 407
DB 472 LQRLHEYTELEDERNERALAAAKKLE-GDLKDLQADSIAKGREAIKQRLKQA 530
QY 408 YLEAIRKNIE-----WLKHKHKKGNKEDYDLSKMRDFI-----NKQADAYVEK 450
DB 531 QMKDFQRELEADARSDRBEIFATAKENKKAASLEADLMQLQEDLAAAEARARKQAD----- 585
QY 451 GILDKKEE 457
DB 586 --LEKEE 590

RESULT 11

US-09-914-259-17
; Sequence 17, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-914-259-17

Query Match 6.6%; Score 158.5; DB 4; Length 956;
Best Local Similarity 20.2%; Pred. No. 0.0015;
Matches 105; Conservative 89; Mismatches 166; Indels 159; Gaps 25;

QY 25 GSQDKSLNR-----ELSAERPLNEQIAEAEDKTKTYPPENKPGOSNYSFVDNLL- 78
DB 321 GORAKTIKNTVSNLELTAE-----EWKKYKEKEKNKALKSVLQHLEML 367
QY 79 -----RAITEKEKE-KEROSIRSSPLDNKLNVED-----VDSTKNRKLIDDYDSTKSG 127

DB 368 NRWRNGEAVPEDEQISAKDHKSL--EPCDNTPIIDNITPPVVDGISAER--EKYDEEITSL 423
QY 128 DHKQDDPDGLHOLDGTPLTAEIDIVHKIAARIYEND-----RAVEDKIVSKLLNGLIT 182
DB 424 YRQDDDKDDEINQ-----OSQLAEKLUQMLQDDELLASTRRDYEKIQEELRLQIEN 476
QY 183 ESOAHTLEDEVAEVLQKLISKEANNYE---EDPNKPTSWTENQAGKIPEKVTPTMAAIQDG 239
DB 477 EA---AKDEVKEVLQAL-EELAVNYDQKSOEVEDKTRANEQLTDELAQKTTTLTTTQRE 531
QY 240 LAK-----GENDETVSNLTLTNGLERRTKTYSED 269
DB 532 LSQQLSLSNHHOKRATETILNLLKDLGIGIGICTND---VKTLADVNGVTEEEFTMAR- 587
QY 270 NFRDFOYFNPYALLKSTI-----DSEKEAKEKETLITIMKTLIDFVKMVKYK 317
DB 588 ---LYISKMKSEVKSLSVNRSKOLESQMSNRKKNASERELAACQLLISOHEAKIKSL 642
QY 318 TISPESGVSYLENLDEMIALQTKNLEK---NATDNISKLPAPSEKSEET--DSTKEE 372
DB 643 T-----DYQNMW---QKRRQLEESQDLSSEELAKL--RAQEKMHVSVFQDKEKEH 688
QY 373 AAKMEKEGSLKSTKDDNSNPGGKTDEPKGTAYLEAIRKNIEWLKHDKKGNKEDYD 432
DB 689 LTRLQ-----DAEEVKALEQQMESHR-----EAHOKQ----- 716
QY 433 LSKMRDFINKQADAYVEKGILDK---EAEAIKRIYSSIL 468
DB 717 LSLRLDEEEKORIIDEIRDLNQLQLEQERLSSDYNKL 755

RESULT 12

US-09-308-375-2
; Sequence 2, Application US/09308375
; Patent No. 6300117
; GENERAL INFORMATION:
; APPLICANT: Genencor
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms
; FILE REFERENCE: GC394-PCT
; CURRENT APPLICATION NUMBER: US/09/308,375
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: EP9719636.4
; EARLIER FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2285
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-308-375-2

Query Match 6.6%; Score 158; DB 4; Length 2285;
Best Local Similarity 23.8%; Pred. No. 0.0033;
Matches 100; Conservative 61; Mismatches 171; Indels 88; Gaps 16;

QY 85 EKIEKEROISRS--SPLDNKLNVEDVDSTKNKRLIDDYDSTKSGLDHKKPQDDPDGLHOLD 142
DB 1014 DNAKADLSLLETYSKSDSIDVFKMSFDKAGKNKIDGKSLSSVKSEVGDGLGEYLAEG 1073
QY 143 GTPLTAEDI-----VHKIAARIYENDRAVFDKIVSKLLNGLITESQAHTLE 190
DB 1074 N---EAEDFGKKLKEALDANSVDDIKAAIKEMSDAMQFDS--VODVLNGIDFNNT-----K 1124
QY 191 DEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMA---AIQDGLAKGENDE 247
DB 1125 DQVAP-LNDLLEKMAEG-----KSISANEANTLIQDKELAQAISIENGVVVKINRDE 1175
QY 248 -----TVSNLTLTNGLERRTKTYSEDNFRDFOYFNPYALLKSIDSEK 291
DB 1176 VIKQKRVKLDAYNDVMVTSNKLUMKTE-VNNAIKTLNADTLR-----IDSLK 1220
QY 292 EAKEKETLITIMKTLIDF-VKMVKYGTISPESGVSYLENLDEMIALQTKNLEKNATDN 350

Db 1221 KLRKRLDMSAEALSLEVKSINNADAKK-----LKKLEKMK-----LQPGGYSN 1268
Qy 351 ISKLFPPAPSEKS-----HEETDSTKEAAKMEKEYGSLKSTKDDNSNPGKTDPEK 402
Db 1269 -SQJEAQMSYSALEYSASEATSTQEMNKQALVEAGTSLNWTDOQEKANETKYSM 1327
Qy 403 GKTAYLEATKNTWELKKHDKKGNKEDYDLSKMRDFINKQADAYVEKGILDKBEAIAK 462
Db 1328 YVVDKYEALEKVAEIDKYNQVDPKYSQYRDAIKKEIKALQKQKLLMQEQAKLLK 1387
RESULT 13
US-08-533-306A-4
; Sequence 4, Application US/08533306A
; Patent No. 5837457
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/533,306A
; FILING DATE: September 25, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869COB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-533-306A-4

Query Match 6.6%; Score 157.5; DB 2; Length 885;
Best Local Similarity 22.8%; Pred. No. 0.0016;
Matches 110; Conservative 80; Mismatches 183; Indels 109; Gaps 22;
Qy 31 LHNRELSAERPLNEQIAEAEDKIKKTYPPENKPGQSNYSFV--DNLNLLRAITEKEKTE 88
Db 232 LQNEVESVTGMLE--AEGKAIKADKVASLSOLODTQELQOETROKLVNSTKLRLQLE 289
Qy 89 KERQSTR---SSPLDNKLNVEDVDSTKN-----RKLDDYDSTKSGLDH---KFQDDPD 136
Db 290 EERNLSQDLDEMEAKQNLERHISTLNLQSDSKKLQDFASTVEALEEGKRRFQKETE 349
Qy 137 GLHOLDGTPLTAEIDVHKIAARIYEENDRAVFD-----KIVSKLLNLGLITSQAHTLED 191
Db 350 NLTQQVEEKAAYDKLEKTKNRLQOELDLVVDLQNRQLVSNL-----EKKQRKFDQ 402
Qy 192 EYAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPEKVTPTMA-ATODGL-AKGENDETV 249
Db 403 LLAE--EKNIS--SKYADERDR---AEAAREKETKALSRLAREALEAKEELERT- 452

Qy 250 SNTLTLNGLERKTKTYSSEDFRDFQYFPNFYALLKSIDS-----EKEAKKETLIT 301
Db 453 -----NKMUKAEMD-----LVSSKDDVGKVVHLEKSKRALETOME 489
Qy 302 IMKTLIDFVMMVKYGTISPEEGVSYLENLDEMIALQTKNKLKKNATDNISK-----L 354
Db 490 EMKTLQLEDELDQ-----ASEDAKLRLEVNMQALKGQFERDLQARDQNEEKRRQLRQL 545
Qy 355 FPAPSEKSHETDSTKEEAAMEKEYGSLKSDKDDNSNPGGKTDEPK--GKTAYLEAI 412
Db 546 HEYETELEDERNERALAAAKKLE-GDLKDLLELQADSAIKGREAIKQLRKLOAQMKDF 604
Qy 413 RKNIE-----WLKKHDKKGNKEDYDLSKMRDFI-----NKQADAYVEKGILDK 455
Db 605 ORELEDARASDEIFATAKNERKAKSLEADLMQLQEDLAAAEARKQAD-----LEK 657
Qy 456 EE 457
Db 658 EE 659

RESULT 14

US-08-742-923A-4
; Sequence 4, Application US/08742923A
; Patent No. 5869611
; GENERAL INFORMATION:
; APPLICANT: Liu, Pu
; APPLICANT: Collins, Francis S.
; APPLICANT: Siciliano, Michael J.
; APPLICANT: Claxton, David
; TITLE OF INVENTION: Markers for Detection of Chromosome 16
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/742,923A
; FILING DATE: NO. 5869611ember 1, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-00869DVC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 641-1600
; TELEFAX: (810) 641-0270
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 885 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-742-923A-4

Query Match 6.6%; Score 157.5; DB 2; Length 885;
Best Local Similarity 22.8%; Pred. No. 0.0016;
Matches 110; Conservative 80; Mismatches 183; Indels 109; Gaps 22;
Qy 31 LHNRELSAERPLNEQIAEAEDKIKKTYPPENKPGQSNYSFV--DNLNLLRAITEKEKTE 88
Db 232 LQNEVESVTGMLE--AEGKAIKADKVASLSOLODTQELQOETROKLVNSTKLRLQLE 289

QY 89 KERQSI--SSPLDNKLNVDVSTKN-----RKLIDDDYDSTKSGLDH--KFQDDPD 136
Db 290 EERNISQQLDDEMEAKQNLHRTLNQLSDSKKLQDPASTVEALEEGKRFQKE 349
QY 137 GLHOLDGTPLTAEIVHKIARIYEENDRAVFD-----KIYSKLLNLGLITESQAHTLED 191
Db 350 NITQOYEKAAYDKLETKNKLQELDOLVVDLNDQRLVSNL-----EKKORKFDQ 402
QY 192 EYAEVLQKLISKEANNYEDPNKPTSWENOAGKIPEKVTMA--AIQDGL-AKGNDETV 249
Db 403 LLAE--ERNIS--SKYADERD--AAEAAREKETALSILARALEALEKELEERT- 452
QY 250 SNTLTLTNGLERRTYSEDNFRDQYFPNFYALKSIDS-----EKAKEKETLIT 301
Db 453 -----NKLKAEMED-----LVSSKDDVGNVHELEKSKRALETQME 489
QY 302 IMKTLIDFVMMVKYGTISPESGVSYLENLDEMIALQTKNLEKNATNISK-----L 354
Db 490 EMKTLQLELEDELQ-----ASEDAKLRLVYNMQALKGQFERDQARDEQNEEKRRLQRL 545
QY 355 FPAPSEKSHETDSTKEEAAMEKEYGSLKDDSTKDDNSNPGGKTDEPK--GKTEAYLEAI 412
Db 546 HEYTELEDERNERALAAAKKLE--GDLKDLQADSAIGREAIKQLRLQAKMDF 604
QY 413 RKNIE-----WLKKHDKGNKEDYDLKSMRDFI-----NKQADAYVERGILDK 455
Db 605 QRELEDAASRDEIFATAKENEKAKSLEADLWMLQEDLAAERARKQAD-----LEK 657
QY 456 EE 457
Db 658 EE 659

RESULT 15
US-08-685-871-2
; Sequence 2, Application US/08685871
; Patent No. 6013499
; GENERAL INFORMATION:
; APPLICANT: NARUMIYA, Shuh
; APPLICANT: IWAMATSU, Akihiro
; NUMBER OF INVENTION: RHO TARGET PROTEIN KINASE P160
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,871
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-184102
; FILING DATE: 25-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-262553
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16887/845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1354 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-685-871-2

Query Match 6.5%; Score 155; DB 3; Length 1354;
Best Local Similarity 21.0%; Pred. No. 0.0043;
Matches 104; Conservative 95; Mismatches 181; Indels 116; Gaps 23;

QY 26 SODKSLHNRLELSAERPLNEQIAEA-----BED-----KIKKTYPPNKKPGQSNYSFVDNLN 76
Db 530 SONSOLANEKLS--QLQKQLEANDLLRTESDTAVLRKSHITEMSK-----SISQLESIN 582
QY 77 LLRAATEKEKTEKERSIRSS--PLDNKNLVNEDVDSTKNRKLIDDDYDSTKSGLDHKKFD 133
Db 583 --RELQERNRILENSKSDTKDYQLOAILLEAERDRGHDSEMIQDLQARITSLQEEVKH 640
QY 134 DPDLGHLQDGTPLTAEDIVHKIARIYEENDRAVFDKIVSKLLNLGLITESQAHTLEDEV 193
Db 641 LKHNLKVEGERKEAQMMLN-----HSEKEKNLE-----IDLNYKLKSLQORLEQEV 688
QY 194 AE--VLOKLISKEANNYEE-----DPNKPTSWENOAGKIPEKVTMAAIQ 237
Db 689 NEHKVTKARLTDKHQSIEEAKSVAMCEMEKKLEEREAREKAENRVVQI-EKQCSMLD 747
QY 238 -----DGLAKGENDETVSNLTITNGLERR-----TKTISEDNFRDQYFP 278
Db 748 LKSOOKLEHLTGNKERMEDEVKNLTQLEQESNKRLLQLNELKQAFEDN----- 799
QY 279 NFYALLKSIDSEKAKEKETLITIMKTLIDF--VKMMVKYGTISP-----EGVSYL 328
Db 800 -----LKGL--EKQMKQEIINTLLEAKRLLEFELAQLTQYRGNEGOMRELQDLEAEQYF 852
QY 329 ENLDEMIALQTKNLEKNATNISKLPAPSEKSH-----EETDSTKEEA--MEKE 379
Db 853 STLYKTQVKELKEEIEEKNRENKKTQELQNEKETLATQDLAETKAESEQLARGILLEQ 912
QY 380 YGSL-KDSTKDDNSNPGGKTDEPKGKTEAYLE-----AIRKNIEWLKKHDK-----KGNK 428
Db 913 YFELTQESKKAASRRQEIITD--KQHTVSRLEEANSMLTKDIEILRRNEELTEKMKKAE 970
QY 429 EDYDLSKMRDFINKQA 444
Db 971 EYKLEKEEIEISNLKA 986

Search completed: August 28, 2003, 10:25:12
Job time : 44 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 05:01:52 ; Search time 145 Seconds
(without alignments)
6139.792 Million cell updates/sec

Title: US-09-554-945B-1

Perfect score: 2017

Sequence: 1 taaagctacgccttgcgc.....tcaatccttccactgtc 2017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 1	86.2	4.3	7218	1 US-08-232-463-14	Sequence 14, Appl
2	52.4	2.6	19124	2 US-08-487-826B-13	Sequence 13, Appl
3	48.8	2.4	3384	3 US-08-923-992A-5	Sequence 5, Appl
4	48.6	2.4	7218	1 US-08-232-463-14	Sequence 14, Appl
5	48.2	2.4	2277	1 US-08-676-967-2	Sequence 2, Appl
6	48.2	2.4	2277	1 US-08-676-974-2	Sequence 2, Appl
7	48.2	2.4	2277	1 US-09-098-487-2	Sequence 2, Appl
8	45.6	2.3	2617	1 US-08-430-024-1	Sequence 1, Appl
9	45.6	2.3	2617	1 US-08-782-009-1	Sequence 1, Appl
10	45.6	2.3	2617	3 US-09-017-302-1	Sequence 1, Appl
11	45.6	2.3	3730	1 US-08-242-932-8	Sequence 8, Appl
12	45.6	2.3	3730	1 US-08-714-481-8	Sequence 8, Appl
13	45.6	2.3	3730	5 PCT-US95-06111-8	Sequence 8, Appl
14	45.6	2.3	4200	1 US-08-242-932-1	Sequence 1, Appl
15	45.6	2.3	4200	1 US-08-714-481-1	Sequence 1, Appl
16	45.6	2.3	4200	3 US-08-923-992A-1	Sequence 1, Appl
17	45.6	2.3	4200	5 PCT-US95-06111-1	Sequence 1, Appl
18	43.6	2.2	1295	4 US-09-286-981B-20	Sequence 20, Appl
19	43.4	2.2	289	3 US-09-007-005-17	Sequence 17, Appl
20	43.4	2.2	289	3 US-09-244-796-17	Sequence 17, Appl
21	43.4	2.2	861	4 US-09-601-198-66	Sequence 66, Appl
22	43.2	2.1	5361	3 US-08-973-462-2	Sequence 2, Appl
23	43.2	2.1	6152	3 US-08-973-462-1	Sequence 1, Appl
24	43	2.1	1436	4 US-08-961-527-327	Sequence 327, Appl
25	43	2.1	152331	3 US-09-128-155-16	Sequence 16, Appl
26	42.8	2.1	6755	3 US-08-931-999-4	Sequence 4, Appl
27	42.4	2.1	754	4 US-09-286-981B-21	Sequence 21, Appl

Query Match 4.3%; Score 86.2; DB 1; Length 7218;

ALIGNMENTS

RESULT 1

US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; / MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PT99pt-Fls
; US-08-232-463-14

Sequence 67, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 193, App
Sequence 191, App
Sequence 189, App
Sequence 187, App
Sequence 185, App
Sequence 184, App
Sequence 1, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 70, Appl


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Db 412 GCGCNGTNTYNGARTNAAYATHCCNMGNAAACCCNGAYGGNAAATATGNGGNTTYG 471
QY 1423 TATGAACTTGAAGGATCCACAAAAGATGATACTCCACCCAGGAGGAAAGACAT 1482
Db 472 TTYGNCARTTYAARAYTYNTNGARGCNGNAAAGCNYTNAARGGNATGAAYATGAAR 531
QY 1483 GAACCAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1542
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QY 1543 AAGAACATGACAAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1602
Db 592 ACNCARWNGTNGWNGNACNGTNGCNGTNGAYTGGCNGTNGCNGNAAARGAAYARTY 651
QY 1603 ATCAATAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1662
Db 652 GTNAARAARGGNMGWNGNACNGTNGCNGTNGAYTGGCNGTNGCNGNAAARGAAYARTY 711
QY 1663 G 1663
Db 712 G 712

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RESULT 7

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US-09-098-487-2
; Sequence 2, Application US/09098487
; Patent No. 5917025
; GENERAL INFORMATION:
; APPLICANT: COLLINS, Kathleen
; TITLE OF INVENTION: Human Telomerase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Science & Technology Law Group
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,487
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman Ph.D., Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UCB96-055
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-098-487-2

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Query Match 2.4%; Score 48.2; DB 2; Length 2277;
Best Local Similarity 27.8%; Pred. No. 0.0048;
Matches 167; Conservative 78; Mismatches 356; Indels 0; Gaps 0;
QY 1063 GAAAGGAGAACTAAACCTACAGTGAACACACTTTAGGACTTCCATATATTCCTCAAT 1122
Db 112 GARAARGGNWNAAGGNTGNGGNTTYGNTYNGAATGNTYNGAATGNTYNGAATGNTY 171
QY 1123 TTCTATGCGCTACTGAAAGTATTGATTCAGAAAAAGGAAAGGAAAGGAAAGGAAAG 1182

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Db 172 GTNCARMGNGCNYTNAARGARATHACNACNACNTTYTGARGGNTGYAARATHAAVYTNACNG 231
QY 1193 ATTACTATCATGAAAACACTGATTCAGCTTTGTGAAGATGATGGTGAATAATGGAACAATA 1242
Db 232 GCNAAARAARAYTYNMGNAAARACNAAARGAARAGGNAARAAYTGARAAYWSNGARTGY 291
QY 1243 TCTCCAGAGAGAGGTGTTTCCCTTACCTTGAAACTTTGGATGAAATGATTCCTCTCAGACC 1302
Db 292 CCNAAARAARGARCCNAAARGCNAARAARGCNAARGTNGCNGAYAAARAAGCNGNTNATH 351
QY 1303 AAAACAAGCTAGAAAAAATGCTACTGACATATATAAGCAAGCTTTTCCAGCAGCATCA 1362
Db 352 ATHMGNAAAYTYNWSNTTYAARTGYWSNGARGAYGAYTYNAAARACNCTNTTYGCNCARTY 411
QY 1363 GAGAAGACTCATGAGNAACACAGACAGTACCAGGAAGAGCAGCTTAAGATGAAAGGAA 1422
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QY 1423 TATGAACTTGAAGGATTCACAAAAGATGATACTCCACCCAGGAGGAAAGACAGAT 1482
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QY 1543 AAGAACATGACAAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 1602
Db 592 ACNCARWNGTNGWNGNACNGTNGCNGTNGAYTGGCNGTNGCNGNAAARGAAYARTY 651
QY 1603 ATCAATAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAA 1662
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QY 1663 G 1663
Db 712 G 712

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RESULT 8

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US-08-430-024-1
; Sequence 1, Application US/08430024
; Patent No. 5644030
; GENERAL INFORMATION:
; APPLICANT: Paulmann, Ervin L
; TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF
; TITLE OF INVENTION: AN IGA BINDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,024
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/677,209
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: BL-1
; TELECOMMUNICATION INFORMATION:

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Db          1031  AAAAAAGAGATCCCGAAGTAAAGGTTCCGTGAAGAACTAGGTAAAC 1076

RESULT 9
US-08-782-009-1
; Sequence 1, Application US/08782009
; Patent No. 5714334
; GENERAL INFORMATION:
; APPLICANT: Faulmann, Ervin L
; TITLE OF INVENTION: NOVEL GENE AND METHOD FOR PRODUCTION OF
; TITLE OF INVENTION: AN IgA BINDING PROTEIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/782,009
; FILING DATE: 07-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,024
; FILING DATE: 27-APR-1995
; APPLICATION NUMBER: US 07/677,209
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: BL-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus agalactiae
; STRAIN: DL471
; IMMEDIATE SOURCE:
; CLONE: pELF26
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 320..430
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 320..1510
; OTHER INFORMATION: /codon_start= 320
; OTHER INFORMATION: /function= "binds to Fc region of human
; OTHER INFORMATION: /product= "IgA binding protein"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
; FEATURE:
; NAME/KEY: RBS
; LOCATION: 307..311
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 887..1507
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /bound_moiety= "IgA Fc"
; OTHER INFORMATION: /evidence= EXPERIMENTAL

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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-242-932-1

Query Match 2.3% Score 45.6; DB 1; Length 4200;
Best Local Similarity 45.3%; Pred. No. 0.034;
Matches 211; Conservative 0; Mismatches 249; Indels 6; Gaps 1;
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-714-481-1

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QY 1213 GTGAGATGATGGTGAATATGGAACAATATCTCCAGAAAGGTGTTTCTACTTGAA 1272
DB 671 CTAAGAAATGATGGTGAATATGGAACAATATCTCCAGAAAGGTGTTTCTACTTGAA 730

QY 1273 AACTTGGATGAATGATGCTTCCAGACCAAAACAGCTAGAAAATGCTACTGAC 1332
DB 731 AAAATTGATGAACAATGATCTGATGCAATTTAGAAATCAATTTAACGAA 790

QY 1333 AATTAAGCAAGCTTTTCCAGACCAATCAAGAGAGTCTAGAAACAGACAGTACC 1392
DB 791 ACTAATAGACTGTTACACATCAACAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 850

QY 1393 AAGGAAGAAGCAGCTAAGATGGA-----AAGGAATATGGAAGCTTGAAGGATCCACA 1446
DB 851 CAACAGAAACTCTGAACAGTCAAGATCAAGAGTGAAGAGTGAAGAGTGAAGAG 910

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DB 971 GATAAGATCTATGCTGAAAATATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1030

QY 1567 AAGAAGATGATGACCTTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
DB 1031 AAAAAAGAGAGTCCGAGAGTGAAGGTTGCGTGAAGAGAGAGAGAGAGAGAGAG 1076

RESULT 15

US-08-714-481-1
Sequence 1, Application US/08714481
Patent No. 5766606
GENERAL INFORMATION:
APPLICANT: Brady, L. Jeannine
TITLE OF INVENTION: Cloning of No. 5766606-IgA Fc Binding Forms of
TITLE OF INVENTION: the Group B Streptococcal Beta Antigens
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,481
FILING DATE: 16-SEP-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/242,932
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF142

TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-714-481-1

Query Match 2.3% Score 45.6; DB 1; Length 4200;
Best Local Similarity 45.3%; Pred. No. 0.034;
Matches 211; Conservative 0; Mismatches 249; Indels 6; Gaps 1;
SEQUENCE CHARACTERISTICS:
LENGTH: 4200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-714-481-1

QY 1153 GAAAGAAGCAAAAGAGAAAGAACTGATCTATCTATCATGAAACACTGACTTTT 1212
DB 611 GAAACATCTGCCACTGATCTGGAACGAGAGAAACAATTAACAATAAT 670

QY 1213 GTGAGATGATGGTGAATATGGAACAATATCTCCAGAAAGGTGTTTCTACTTGAA 1272
DB 671 CTAAGAAATGATGGTGAATATGGAACAATATCTCCAGAAAGGTGTTTCTACTTGAA 730

QY 1273 AACTTGGATGAATGATGCTTCCAGACCAAAACAGCTAGAAAATGCTACTGAC 1332
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QY 1333 AATTAAGCAAGCTTTTCCAGACCAATCAAGAGAGTCTAGAAACAGACAGTACC 1392
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QY 1393 AAGGAAGAAGCAGCTAAGATGGA-----AAGGAATATGGAAGCTTGAAGGATCCACA 1446
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QY 1507 TATTGGAAGCCATCAAAAATATTTGAATGTTGAAGAGAGAGAGAGAGAGAGAGAG 1566
DB 971 GATAAGATCTATGCTGAAAATATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1030

QY 1567 AAGAAGATGATGACCTTTCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1612
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Search completed: August 28, 2003, 08:26:05
Job time: 147 secs

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; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
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; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 66
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-931-836-66

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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 142 TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCCACACCCACCTCCTGGCTCTTCCCTGT 201
Db 121 TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCCACACCCACCTCCTGGCTCTTCCCTGT 180

QY 202 TTTTACTCTCCTCTTTTCATTATACAAAGCTACAGTCCAGAGCCAGCGCGGGCT 261
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QY 262 GTGACCCAAAGCGAGCGTGGAAAGATGGGGTTCCCTCGGACCGGCACCTTGATTTCTGTG 321
Db 241 GTGACCCAAAGCGAGCGTGGAAAGATGGGGTTCCCTCGGACCGGCACCTTGATTTCTGTG 300

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QY 1582 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1641
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QY 1642 CTTGACAGGAAAGCCGAGGCCATCAAGCCATTTATAGCAGCCGTGTAATAATGCGCAA 1701
Db 1621 CTTGACAGGAAAGCCGAGGCCATCAAGCCATTTATAGCAGCCGTGTAATAATGCGCAA 1680
QY 1702 AAGATCAGGAGCTTTCACTGTTTCAGAAAAATATATAGCTTTAAACACTTCTAAT 1761
Db 1681 AAGATCAGGAGCTTTCACTGTTTCAGAAAAATATATAGCTTTAAACACTTCTAAT 1740
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Db 1741 TCTGTGATTAATATTTTTCAGCCCAAGGGTTATTAGAAAGTGCATTTACAGTACTTA 1800
QY 1822 ACCTTTTACAAGTGGTTTAAACATAGCTTTTCTCCCGTAAAAAACTATCTGAAAGTAAAGT 1881

RESULT 2

US-10-035-977-66
; Sequence 66, Application US/10035977
; Publication No. US20030134327A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C10
; CURRENT APPLICATION NUMBER: US/10/035,977
; CURRENT FILING DATE: 2001-12-26
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
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; PRIOR APPLICATION NUMBER: 60/135750

Db 1801 ACCTTTTACAAGTGGTTTAAACATAGCTTTCTCCCGTAAAAACTATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAAA 1876

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; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
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; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 66
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-035-977-66

Query Match      92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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|||||
61  GACTTGACTCCCGCGCGCCCAACCCCTGTATTCCTTTGACCCGTGCGAGTGTCTAGAGATCC 120
QY      142  TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCAACCCCTCTCTGGCTCTTCTGCTTCTCTGT 201
|||||
121  TGCAGCGCGCCAGTCCCGCGCCCTCTCCCGCCCAACCCCTCTCTGGCTCTTCTGCTTCTCTGT 180
QY      202  TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 261
|||||
181  TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
QY      262  GTGACCCCAAGCGAGCGTGTGAAGATGGGGTTCCTCGGAGCGGCGACTTTGGATTTCTGGTG 321
|||||
241  GTGACCCCAAGCGAGCGTGTGAAGATGGGGTTCCTCGGAGCGGCGACTTTGGATTTCTGGTG 300
QY      322  TTAGTGTCTCCGATTCAGCTTTCCCAACCTGGAGGAGCGCAAGCAAAATCTCTACAT 381
|||||
301  TTAGTGTCTCCGATTCAGCTTTCCCAACCTGGAGGAGCGCAAGCAAAATCTCTACAT 360
QY      382  AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAACAGCAAGAAAC 441
|||||
361  AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAACAGCAAGAAAC 420
QY      442  AAGATTAAAAAACAATATCTCCAGAAACAAGCAGGTGAGAGCAACTATTCTTTGTT 501
|||||
421  AAGATTAAAAAACAATATCTCCAGAAACAAGCAGGTGAGAGCAACTATTCTTTGTT 480
QY      502  GATAACTTGAACCTGCTAAGGGCAATAACAGAAAAAGAAAAATTTGAGAAAAAGAAACAA 561
|||||
481  GATAACTTGAACCTGCTAAGGGCAATAACAGAAAAAGAAAAATTTGAGAAAAAGAAACAA 540
QY      562  TCTATAAGAAGCTCCCACTTTGATAATTAAGTTGAATGTGAAGATGTTGATTTCAACCAAG 621
|||||
541  TCTATAAGAAGCTCCCACTTTGATAATTAAGTTGAATGTGAAGATGTTGATTTCAACCAAG 600
QY      622  AATCGAAAACGATCGATGATTATGACTCTACTAGAGTGGATGGATGATTAATTTCAA 681
|||||
601  AATCGAAAACGATCGATGATTATGACTCTACTAGAGTGGATGGATGATTAATTTCAA 660
QY      682  GATGATCCAGATGGTCTTTCATCACTAGACGGGACTCCTTTAAACCGCTGAAGACATGTC 741
|||||
661  GATGATCCAGATGGTCTTTCATCACTAGACGGGACTCCTTTAAACCGCTGAAGACATGTC 720
QY      742  CATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTGTTTGACAAGATGTT 801
|||||
721  CATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTGTTTGACAAGATGTT 780
QY      802  TCTAAACTACTTAATCTCGGCTTTATCAGAAAAAGCAACACATACACTGGAAGATGAA 861
|||||
781  TCTAAACTACTTAATCTCGGCTTTATCAGAAAAAGCAACACATACACTGGAAGATGAA 840
QY      862  GTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAGCCCAACAATATGAGGAGGATCCC 921
|||||
841  GTAGCAGAGGTTTACAAAAATTAATCTCAAAGGAGCCCAACAATATGAGGAGGATCCC 900
QY      922  AATAGCCCAACAGCTGAGTGAATCAGCTGGAATAATACCAGAGAAGTGAAGTCCA 981
|||||
901  AATAGCCCAACAGCTGAGTGAATCAGCTGGAATAATACCAGAGAAGTGAAGTCCA 960
QY      982  ATGCGAGCAATCAAGATGCTTTGCTTAAGGAGAAAAACGATGAACAGATGATCTAACACA 1041
|||||
961  ATGCGAGCAATCAAGATGCTTTGCTTAAGGAGAAAAACGATGAACAGATGATCTAACACA 1020
QY      1042  TTAACCTTGACAAATGCTTTGGAAGAGAGAACTTAAACCTACAGTGAAGCAACTTTAGG 1101
|||||
1021  TTAACCTTGACAAATGCTTTGGAAGAGAGAACTTAAACCTACAGTGAAGCAACTTTAGG 1080
QY      1102  GACTTCCAAATATTTCCCAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAAGAA 1161
|||||
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Db 1081 GAATCCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATTTGATTCAGAAAAAGAA 1140
QY 1162 GCAAAAGAGAAACACTGATTTACTATCATGAAACACACTGATTGACTTTGTTGAAGATG 1221
Db 1141 GCAAAAGAGAAACACTGATTTACTATCATGAAACACACTGATTGACTTTGTTGAAGATG 1200
QY 1222 ATGGTGAATATGGAACAATATCTCCAGAAGAAGTGTTCCTACCTTTGAAAACCTGGAT 1281
Db 1201 ATGGTGAATATGGAACAATATCTCCAGAAGAAGTGTTCCTACCTTTGAAAACCTGGAT 1260
QY 1282 GAATGATGCTCTTCAGACCAAAACACAGCTAGAAAAATGCTACTGACATATAGC 1341
Db 1261 GAATGATGCTCTTCAGACCAAAACACAGCTAGAAAAATGCTACTGACATATAGC 1320
QY 1342 AAGCTTTTCCAGCACCATCAGAGAAGAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA 1401
Db 1321 AAGCTTTTCCAGCACCATCAGAGAAGAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA 1380
QY 1402 GCAGCTAAGATGGAAGGAATATGGAAGCTTTGAAGGATTCACAAAAAGATGATACTCC 1461
Db 1381 GCAGCTAAGATGGAAGGAATATGGAAGCTTTGAAGGATTCACAAAAAGATGATACTCC 1440
QY 1462 AACCAGAGGAAACAGAGATGAACCCAAAGGAAACAGAGCCATTTTGGAAAGCATC 1521
Db 1441 AACCAGAGGAAACAGAGATGAACCCAAAGGAAACAGAGCCATTTTGGAAAGCATC 1500
QY 1522 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAAATATAAGAGATTATGAC 1581
Db 1501 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAAATATAAGAGATTATGAC 1560
QY 1582 CTTTCAAAAGATGAGAGCTTCATCAATAAACAAGCTGATGCTTTATGTGGAGAAAGCATC 1641
Db 1561 CTTTCAAAAGATGAGAGCTTCATCAATAAACAAGCTGATGCTTTATGTGGAGAAAGCATC 1620
QY 1642 CTTGACAGGAAAGACCGAGCCATCAAGCCATTTATAGCAGCTGTAAAAATGGCA 1701
Db 1621 CTTGACAGGAAAGACCGAGCCATCAAGCCATTTATAGCAGCTGTAAAAATGGCA 1680
QY 1702 AAGATCCAGGAGCTTTCAACTGTTTCAGAAAAACATATATAGCTTAAAAACACTTCTAAT 1761
Db 1681 AAGATCCAGGAGCTTTCAACTGTTTCAGAAAAACATATATAGCTTAAAAACACTTCTAAT 1740
QY 1762 TCTGTGATTAATAATTTTGGCCCAAGGGTTATTAGAAAGTCTGAAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATAATTTTGGCCCAAGGGTTATTAGAAAGTCTGAAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAAGTGTAAACATAGCTTTCTCCCGTAAAAACATATCTGAAAGTAAAGT 1881
Db 1801 ACCTTTTACAAGTGTAAACATAGCTTTCTCCCGTAAAAACATATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 3

US-10-063-735-149
; Sequence 149, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735

; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 149
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-063-735-149

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGGCTCAGAGAACTTCAGACACCCACAGGCGGACAGCGTCCCTCTTACCTGGA 81
Db 1 GTCTCCGGCTCAGAGAACTTCAGACACCCACAGGCGGACAGCGTCCCTCTTACCTGGA 60
QY 82 GACTTGACTCCCGCGCGCCCAACCTTGCTTATTCCTTTCAGCGTGCAGTGTGAGATCC 141
Db 61 GACTTGACTCCCGCGCGCCCAACCTTGCTTATTCCTTTCAGCGTGCAGTGTGAGATCC 120
QY 142 TGCAGCGCCCAAGTCCCGCGCCCTCTCCCGCCCCACACCCACCTCTTGGCTTCTCTGT 201
Db 121 TGCAGCGCCCAAGTCCCGCGCCCTCTCCCGCCCCACACCCACCTCTTGGCTTCTCTGT 180
QY 202 TTTTACTCTCTCTTTTTCATTATACAAAAAGCTACAGCTCCAGGAGCCCGCGCGGCT 261
Db 181 TTTTACTCTCTCTTTTTCATTATACAAAAAGCTACAGCTCCAGGAGCCCGCGCGGCT 240
QY 262 GTGACCCAAAGCGGCGGTGGAAGATTTGGGTTCTCGGACCGGCACTTTGGATTTCTGGTG 321
Db 241 GTGACCCAAAGCGGCGGTGGAAGATTTGGGTTCTCGGACCGGCACTTTGGATTTCTGGTG 300
QY 322 TTAGTCTCCCGATTCAGCTTTCCCAACCTTGGAGGAAAGCAAGCAAAATCTTACAT 381
Db 301 TTAGTCTCCCGATTCAGCTTTCCCAACCTTGGAGGAAAGCAAGCAAAATCTTACAT 360
QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTTGCTGAAGCAAGAAAGAC 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTTGCTGAAGCAAGAAAGAC 420
QY 442 AAGATTAAAAAACATATCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 501
Db 421 AAGATTAAAAAACATATCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 480
QY 502 GATACTTCAACTCTCTAGGCGCAATAACAGAAAGGAAAGAAATTCAGAAAGAAAGACAA 561
Db 481 GATACTTCAACTCTCTAGGCGCAATAACAGAAAGGAAAGAAATTCAGAAAGAAAGACAA 540
QY 562 TCTATAAGAGCTCCCGACTTTGATATAAGTTGAATGTGAAGATGTTGATTCACCAAG 621
Db 541 TCTATAAGAGCTCCCGACTTTGATATAAGTTGAATGTGAAGATGTTGATTCACCAAG 600
QY 622 AATCGAAAACTGATCGATGATTGACTCTACTAAGAGTGGATTTGGATCATAAATTCAA 681
Db 601 AATCGAAAACTGATCGATGATTGACTCTACTAAGAGTGGATTTGGATCATAAATTCAA 660
QY 682 GATGATCCAGATGGTCTTCATCACTAGACGGGACTCTTAAACCGCTGAAGCATGTC 741
Db 661 GATGATCCAGATGGTCTTCATCACTAGACGGGACTCTTAAACCGCTGAAGCATGTC 720
QY 742 CATATAATCGCTCCCGAGGATTTTGAAGAAAAATGACAGAGCGCTGTTTGAAGAGATGTT 801
Db 721 CATATAATCGCTCCCGAGGATTTTGAAGAAAAATGACAGAGCGCTGTTTGAAGAGATGTT 780
QY 802 TCTAAACTACTTAATCTCGGCTTATACAGAAAGCCAAAGCATACACTGGAAGATGAA 861
Db 781 TCTAAACTACTTAATCTCGGCTTATACAGAAAGCCAAAGCATACACTGGAAGATGAA 840
QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAAAGCCAAATTTAGCAGGAGTCCC 921
Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAAAGCCAAATTTAGCAGGAGTCCC 900

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QY 922 AATAAGCCCAAGCTGGACTGAGAAATACAGGCTGGAAGAAATACAGAGAAAGTGAATCCCA 981
Db 901 AATAAGCCCAAGCTGGACTGAGAAATACAGGCTGGAAGAAATACAGAGAAAGTGAATCCCA 960
QY 982 ATGGCAGCAATCAAGATGGTCTTAAAGGAGAAACGATGAACAGTATCTAACACA 1041
Db 961 ATGGCAGCAATCAAGATGGTCTTAAAGGAGAAACGATGAACAGTATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGGCTTGAAGAGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1101
Db 1021 TTAACCTTGACAAATGGCTTGAAGAGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1080
QY 1102 GACTTCCAAATATTTCCCAAAATTTCTATCGCTACTGAAAGATTTGATTCAGAAAAGAA 1161
Db 1081 GACTTCCAAATATTTCCCAAAATTTCTATCGCTACTGAAAGATTTGATTCAGAAAAGAA 1140
QY 1162 GCAAAGAGAAAGAAACACTGATTACTATCATGAAGAAACACGATGACTTTGTCAAGATG 1221
Db 1141 GCAAAGAGAAAGAAACACTGATTACTATCATGAAGAAACACGATGACTTTGTCAAGATG 1200
QY 1222 ATGGTGAATATGGAACAATATCTCCAGAGAAAGGTGTTCTTACCTTGAAGAACTTTGGAT 1281
Db 1201 ATGGTGAATATGGAACAATATCTCCAGAGAAAGGTGTTCTTACCTTGAAGAACTTTGGAT 1260
QY 1282 GAAATGATTGCTCTTCAGACCAAAACAAAGCTGAAAGAAATGCTACTGACAAATATAGC 1341
Db 1261 GAAATGATTGCTCTTCAGACCAAAACAAAGCTGAAAGAAATGCTACTGACAAATATAGC 1320
QY 1342 AAGCTTTTCCAGCACCACATCAGAGAAGAGTATCAAGAAACACAGACATACCAAGAGAA 1401
Db 1321 AAGCTTTTCCAGCACCACATCAGAGAAGAGTATCAAGAAACACAGACATACCAAGAGAA 1380
QY 1402 GCACCTAAGATGGAAGAAATATGGAAGCTTGAAGATTCACAAAGATGATTAATCC 1461
Db 1381 GCACCTAAGATGGAAGAAATATGGAAGCTTGAAGATTCACAAAGATGATTAATCC 1440
QY 1462 AACCAGGAGAAAGACAGATGAACCCAAAGGAAACACAGAGCTTATTTGGAAGCCATC 1521
Db 1441 AACCAGGAGAAAGACAGATGAACCCAAAGGAAACACAGAGCTTATTTGGAAGCCATC 1500
QY 1522 AGAAAAATATGAAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAATATGAC 1581
Db 1501 AGAAAAATATGAAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAATATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGAGAAAGGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGAGAAAGGCATC 1620
QY 1642 CTTGACAAAGGAAGACGAGGACATCAAGCGCATTTATAGCAGCCTGTAAAGAAATGCAA 1701
Db 1621 CTTGACAAAGGAAGACGAGGACATCAAGCGCATTTATAGCAGCCTGTAAAGAAATGCAA 1680
QY 1702 AAGATCAGAGAGTCTTTCAACTGTTTCAGAAACATATATAGCTTTAAACACTTCTAAT 1761
Db 1681 AAGATCAGAGAGTCTTTCAACTGTTTCAGAAACATATATAGCTTTAAACACTTCTAAT 1740
QY 1762 TCTGTGATTAATAATTTTGAACCAAGGTTTATAGAAAGTGTGAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATAATTTTGAACCAAGGTTTATAGAAAGTGTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCGTTAAACACTATCTGAAAGTAAAGT 1881
Db 1801 ACCTTTTACAAGTGGTTAAACATAGCTTTCTTCCGTTAAACACTATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAGA 1876

```

RESULT 4

US-10-137-870-89

: Sequence 89, Application US/10137870

: Publication No. US20030138883A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C155
 ; CURRENT APPLICATION NUMBER: US/10/137,870
 ; CURRENT FILING DATE: 2002-05-03

; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 89

LENGTH: 1893

TYPE: DNA

ORGANISM: Homo Sapien

US-10-137-870-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY 22 GTCTCCGCTCACAGGAACCTTCAGCACCCACAGGGCGGAGCGCTCCCTCTTACCTGGA 81
Db 1 GTCTCCGCTCACAGGAACCTTCAGCACCCACAGGGCGGAGCGCTCCCTCTTACCTGGA 60
QY 82 GACTTGACCTCCGCGCGCCCAACCTGCTTATCCCTTGACGTCGAGTGTGAGATCC 141
Db 61 GACTTGACCTCCGCGCGCCCAACCTGCTTATCCCTTGACGTCGAGTGTGAGATCC 120
QY 142 TGCAGCGCGCCAGTCCCGGCGCCCTCTCCCGCCACACACCCCTCTCGCTTCCCTGT 201
Db 121 TGCAGCGCGCCAGTCCCGGCGCCCTCTCCCGCCACACACCCCTCTCGCTTCCCTGT 180
QY 202 TTTTACTCTCTCTTTTCAATTCATAAAGCTACAGCTCCAGGAGCCCGCGGGCT 261
Db 181 TTTTACTCTCTCTTTTCAATTCATAAAGCTACAGCTCCAGGAGCCCGCGGGCT 240
QY 262 GTGACCCAGCGGAGCGTGGGAAGATGGGTTCCTCCGGAGCCGCGGCTGTGATTCGTG 321
Db 241 GTGACCCAGCGGAGCGTGGGAAGATGGGTTCCTCCGGAGCCGCGGCTGTGATTCGTG 300
QY 322 TTAGTGTCTCCGATTCAGAGCTTTCCCAAACTGGAGGAAGCAAGCAAAATCTCTACAT 381
Db 301 TTAGTGTCTCCGATTCAGAGCTTTCCCAAACTGGAGGAAGCAAGCAAAATCTCTACAT 360
QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATTTGCTGAAAGCAAGAAC 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATTTGCTGAAAGCAAGAAC 420
QY 442 AAGATTAAGAAACATATCTCCAGAAACAGCGGTCAGACCACTATCTTTGTT 501
Db 421 AAGATTAAGAAACATATCTCCAGAAACAGCGGTCAGACCACTATCTTTGTT 480
QY 502 GATAACTTGAACCTGCTTAAGGCAATTAACAGAAAGGAAAAAATTGAGAAAAAGAACAA 561
Db 481 GATAACTTGAACCTGCTTAAGGCAATTAACAGAAAGGAAAAAATTGAGAAAAAGAACAA 540
QY 562 TCTATAAGAGCTCCCGCACTTGATAAAGTTGAATGTGGAAGATGTGATTCAACCAAG 621
Db 541 TCTATAAGAGCTCCCGCACTTGATAAAGTTGAATGTGGAAGATGTGATTCAACCAAG 600

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Db 541 TCTATAAGAGCTCCCCACTTGATTAATAAGTTGAAGTGTGATTCACCAAG 600
QY 622 AATCGAAACATGATCGATGATATGACTCTACTAAGAGTGGATGCATATAAATTTCAA 681
Db 601 AATCGAAACATGATCGATGATATGACTCTACTAAGAGTGGATGCATATAAATTTCAA 660
QY 682 GATGATCCAGATGGTCTTCATCACTAGACGGGACTCCTTTAACCGCTGGAAGATGTC 741
Db 661 GATGATCCAGATGGTCTTCATCACTAGACGGGACTCCTTTAACCGCTGGAAGATGTC 720
QY 742 CATAAATCGCTGCCAGGATTTATCAAGAAATGACAGAGCCGTGTTTGACAAGATGTT 801
Db 721 CATAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTGTTTGACAAGATGTT 780
QY 802 TCTAACTACTTAATCTCGGCTTATACAGAAAGCCAAAGCACATACACTGGAAGATGAA 861
Db 781 TCTAACTACTTAATCTCGGCTTATACAGAAAGCCAAAGCACATACACTGGAAGATGAA 840
QY 862 GTAGCAGAGGTTTACAAAATTAATCTCAAGGAAGCCAAATATTAGAGGAGATCCC 921
Db 841 GTAGCAGAGGTTTACAAAATTAATCTCAAGGAAGCCAAATATTAGAGGAGATCCC 900
QY 922 AATAGCCCAACAGCTGACATGAGAACTGAGCTGGAATAATACCAGAGAAAGTGACTCA 981
Db 901 AATAGCCCAACAGCTGACATGAGAACTGAGCTGGAATAATACCAGAGAAAGTGACTCA 960
QY 982 ATGGCAGCAATCAAGATGGTCTTGCTAAGGGAGAAACAGATGAACAGTATCTAACACA 1041
Db 961 ATGGCAGCAATCAAGATGGTCTTGCTAAGGGAGAAACAGATGAACAGTATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTTAGG 1101
Db 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTTAGG 1080
QY 1102 GACTTCCAAATATTCCTCAAAATTTCTATCGCTACTGAAAGTATTTGATTCAGAAAAGAA 1161
Db 1081 GAATCCCAATATTCCTCAAAATTTCTATCGCTACTGAAAGTATTTGATTCAGAAAAGAA 1140
QY 1162 GCAAAAGAGAAGAAACACTGATTACTATCATGATGAAACACTGATTGCTTTGTGAAGATG 1221
Db 1141 GCAAAAGAGAAGAAACACTGATTACTATCATGATGAAACACTGATTGCTTTGTGAAGATG 1200
QY 1222 ATGTTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTGAACACTTGGAT 1281
Db 1201 ATGTTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTGAACACTTGGAT 1260
QY 1282 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAATATGCTACTGACAAATATAGC 1341
Db 1261 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAATATGCTACTGACAAATATAGC 1320
QY 1342 AAGCTTTTCCAGACCATCATGAGAAGAGTCTATGAAGAAACAGACAGTACCAGGAAGAA 1401
Db 1321 AAGCTTTTCCAGACCATCATGAGAAGAGTCTATGAAGAAACAGACAGTACCAGGAAGAA 1380
QY 1402 GCAGTAAAGTGAAGAGGAATATGGAAGCTTGAAGATTCACAAAGATGATACTCC 1461
Db 1381 GCAGTAAAGTGAAGAGGAATATGGAAGCTTGAAGATTCACAAAGATGATACTCC 1440
QY 1462 AACCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCTATTTTGGAGGCCATC 1521
Db 1441 AACCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAGCTATTTTGGAGGCCATC 1500
QY 1522 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAAAGATTATGAC 1581
Db 1501 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAAAGATTATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTTGGAGAAAGGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTTGGAGAAAGGCATC 1620
QY 1642 CTTGACAGGAAGAGCGGAGCCATCAAGCGCATTTATAGCAGCCGTGTAATAATGGCAA 1701
Db 1621 CTTGACAGGAAGAGCGGAGCCATCAAGCGCATTTATAGCAGCCGTGTAATAATGGCAA 1680
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QY 1702 AAGATCCAGGAGTCTTTCAACTGTTTCAAGAAACATAATATAGCTTAAAAACACTTCTAAT 1761
Db 1681 AAGATCCAGGAGTCTTTCAACTGTTTCAAGAAACATAATATAGCTTAAAAACACTTCTAAT 1740
QY 1762 TCTGTGATTAATAATTTTTTGACCCCAAGGGTTATTAGAAGTCTGCTGAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATAATTTTTTGACCCCAAGGGTTATTAGAAGTCTGCTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAAGTGGTTAAAAACATAGCTTTCTCCCGTAAAAACCTATCTGAAAGTAAAGT 1881
Db 1801 ACCTTTTACAAGTGGTTAAAAACATAGCTTTCTCCCGTAAAAACCTATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAAA 1876
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RESULT 5

US-10-140-018-89
; Sequence 89, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-018-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 22 GTCTCCGCGTCACAGGAATTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGA 81
Db 1 GTCTCCGCGTCACAGGAATTCAGCACCCACAGGGCGGACAGCGCTCCCTCTACCTGGA 60
QY 82 GACTTGTACTCCCGCGGCCCAACCTGCTTATCCCTTGACCGTGCAGTGTGACAGATCC 141
Db 61 GACTTGTACTCCCGCGGCCCAACCTGCTTATCCCTTGACCGTGCAGTGTGACAGATCC 120
QY 142 TGCAGCGCCCGCAGTCCCGGCCCTCTCCCGCCCAACACCCCTCTCTGGCTCTTCTCTGT 201
Db 121 TGCAGCGCCCGCAGTCCCGGCCCTCTCTCCCGCCCAACACCCCTCTCTGGCTCTTCTCTGT 180
QY 202 TTTTACTCTCTCTTTTCATTAACAAAAGCTACAGCTCCAGGAGCCCGCGGCT 261
Db 181 TTTTACTCTCTCTTTTCATTAACAAAAGCTACAGCTCCAGGAGCCCGCGGCT 240

Qy	262	GTGACCCAAACCGAGCGTGAAGAATGGGGTTCTCGGGACCGGCACCTTGGATCTCTGGTG	321
Db	241	GTACCCAAACCGAGCGTGAAGAATGGGGTTCTCGGGACCGGCACCTTGGATCTCTGGTG	300
Qy	322	TTAGTGTCTCCCGATTCAAGCTTTCGCCAAACCTGGAGGAGCCAAAGCAAAATCTCTACAT	381
Db	301	TTAGTGTCTCCCGATTCAAGCTTTCGCCAAACCTGGAGGAGCCAAAGCAAAATCTCTACAT	360
Qy	382	AATAGAGAAATTAAGTCGAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGAC	441
Db	361	AATAGAGAAATTAAGTCGAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGAC	420
Qy	442	AAGATTAAAAAACAATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGGT	501
Db	421	AAGATTAAAAAACAATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGGT	480
Qy	502	GATAACTTGAACCTGCTAAGGGCAATTAACAGAAAAAGGAAAAAATTGAGAAAAAGAACAA	561
Db	481	GATAACTTGAACCTGCTAAGGGCAATTAACAGAAAAAGGAAAAAATTGAGAAAAAGAACAA	540
Qy	562	TCTATAAGAAAGCTCCCACTTGATATAAGTTGAATGTGGAAGATGTTGATTCACACCAAG	621
Db	541	TCTATAAGAAAGCTCCCACTTGATATAAGTTGAATGTGGAAGATGTTGATTCACACCAAG	600
Qy	622	AATCGAAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTGCGATCATAAATTTCAA	681
Db	601	AATCGAAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTGCGATCATAAATTTCAA	660
Qy	682	GATGATCCAGATGGTCTTCATCACTAGACGGGACTCCTTTAAACCGCTGAAGACATTGTC	741
Db	661	GATGATCCAGATGGTCTTCATCACTAGACGGGACTCCTTTAAACCGCTGAAGACATTGTC	720
Qy	742	CATAAAATCGCTGCCAGGATTTATCAAGAAAATGACAGCGCGTGTGTTGACAAGATTGTT	801
Db	721	CATAAAATCGCTGCCAGGATTTATGAGAAAATGACAGCGCGTGTGTTGACAAGATTGTT	780
Qy	802	TCTAAACTACTTAATCTCGGCTTTATCAGAAAAGCCCAAGCACATACACTGGAAGATGAA	861
Db	781	TCTAAACTACTTAATCTCGGCTTTATCAGAAAAGCCCAAGCACATACACTGGAAGATGAA	840
Qy	862	GTAGCAGAGGTTTTACAAAAATTAATCTCAAGGAAGCCCAACAATTATGAGGAGATCCC	921
Db	841	GTAGCAGAGGTTTTACAAAAATTAATCTCAAGGAAGCCCAACAATTATGAGGAGATCCC	900
Qy	922	AATAGCCCAACAGCTGAGATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA	981
Db	901	AATAGCCCAACAGCTGAGATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA	960
Qy	982	ATGGCAGCAATTCAGATGGTCTTGCTAAGGGAAGAAACAGATGAACAGATATCTAACACA	1041
Db	961	ATGGCAGCAATTCAGATGGTCTTGCTAAGGGAAGAAACAGATGAACAGATATCTAACACA	1020
Qy	1042	TTAACCCTTGACAAATGGCTTGGAAAGGAGAACTAAAAACCTACAGTGAAGACAACTTTAGG	1101
Db	1021	TTAACCCTTGACAAATGGCTTGGAAAGGAGAACTAAAAACCTACAGTGAAGATG	1080
Qy	1102	GACTTCCCAATATTTCCCAATTTCTATGCGCTACTGAAAAGTATGATTGAGAAAAGAA	1161
Db	1081	GACTTCCCAATATTTCCCAATTTCTATGCGCTACTGAAAAGTATGATTGAGAAAAGAA	1140
Qy	1162	GCAAGAGAAAGAAACACTGATTACTATCATGAAAAACACTGATTGACTTTGTGAAGATG	1221
Db	1141	GCAAGAGAAAGAAACACTGATTACTATCATGAAAAACACTGATTGACTTTGTGAAGATG	1200
Qy	1222	ATGCTGAAATATGAAACAATATCTCCAGAGAGAGGTGTTTCCTACCTTGAAAACCTTGGAT	1281
Db	1201	ATGCTGAAATATGAAACAATATCTCCAGAGAGAGGTGTTTCCTACCTTGAAAACCTTGGAT	1260
Qy	1282	GAAATGATTGCTCTTCCAGACCAAAAACAAGCTAGAAAAAATGCTACTGCAATATAAGC	1341
Db	1261	GAAATGATTGCTCTTCCAGACCAAAAACAAGCTAGAAAAAATGCTACTGCAATATAAGC	1320
Qy	1342	AAGCTTTTCCACACCATCAGAGAGAGTCATGAAGAAACAGACAGTACCAAGGAAGAA	1401

[illegible]

RESULT 6

```

US-10-140-021-89
; Sequence 89, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RJC167
; CURRENT APPLICATION NUMBER: US/10/140, 021
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien

```


US-10-140-021-89

Query Match									
Best Local Similarity 92.5%; Score 1866.4; DB 12; Length 1893;									
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;									
QY	22	GTCTCCGCGT	CACAGAACTT	CAGACCCACAGGCGGACAGCGCTCCCTCTACCTGGA	81				
DB	1	GTCTCCGCGT	CACAGAACTT	CAGACCCACAGGCGGACAGCGCTCCCTCTACCTGGA	60				
QY	82	GACTTGACT	CCGCGCGCCCAACCTGCTTATCCCTTGACCGTGCAGATGCC	141					
DB	61	GACTTGACT	CCGCGCGCCCAACCTGCTTATCCCTTGACCGTGCAGATGCC	120					
QY	142	TGCAGCGCG	CAGTCCCGCGCCCTCTCCGCGCCACACCCCTCCCTGCTCTTCTGT	201					
DB	121	TGCAGCGCG	CAGTCCCGCGCCCTCTCCGCGCCACACCCCTCCCTGCTCTTCTGT	180					
QY	202	TTTTTACT	CTCTCTTTTCAATCAATAAAGCTACAGCTCCAGGAGCCAGCGCGGCT	261					
DB	181	TTTTTACT	CTCTCTTTTCAATCAATAAAGCTACAGCTCCAGGAGCCAGCGCGGCT	240					
QY	262	GTGACCCAA	CGGCGGTGGAAGATGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	321					
DB	241	GTGACCCAA	CGGCGGTGGAAGATGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	300					
QY	322	TTAGTGCT	CCCGATTCAAGCTTTCCCAAACTGGAGGAGCAAGCAAACTCTCTACAT	381					
DB	301	TTAGTGCT	CCCGATTCAAGCTTTCCCAAACTGGAGGAGCAAGCAAACTCTCTACAT	360					
QY	382	AATAGAGAA	TTAAGTGCAGAAAGACCTTTGAATGAACAGATGCTGGAAGCAGAAAGAC	441					
DB	361	AATAGAGAA	TTAAGTGCAGAAAGACCTTTGAATGAACAGATGCTGGAAGCAGAAAGAC	420					
QY	442	RAGATTA	AAAAAACAATATCCTCCAGAAACAGCCAGCTCAGCAACTATTTCTTTGT	501					
DB	421	RAGATTA	AAAAAACAATATCCTCCAGAAACAGCCAGCTCAGCAACTATTTCTTTGT	480					
QY	502	GATAACTT	GAACTGCTGCTAAGGCAATAACAGAAAAGGAAAAATTTGAGAAAGAAAGACAA	561					
DB	481	GATAACTT	GAACTGCTAAGGCAATAACAGAAAAGGAAAAATTTGAGAAAGAAAGACAA	540					
QY	562	TCTATAAGA	AGCTCCCGACTTGATTAATAGTTGAATGGAAGATGTTGATTCACCAAG	621					
DB	541	TCTATAAGA	AGCTCCCGACTTGATTAATAGTTGAATGGAAGATGTTGATTCACCAAG	600					
QY	622	ATTCGAA	AACTCATCTGATGATGCTACTAGAGTGGATGGATCATATAATTTCAA	681					
DB	601	ATTCGAA	AACTCATCTGATGATGCTACTAGAGTGGATGGATCATATAATTTCAA	560					
QY	682	GATGATCC	AGATGGTCTTCACTCACTAGACGGGACTCCTTTAACCGCTGAAGACATTTGC	741					
DB	661	GATGATCC	AGATGGTCTTCACTCACTAGACGGGACTCCTTTAACCGCTGAAGACATTTGC	720					
QY	742	CATAAAAT	CGCTGCCAGGATTTATGAAGAAATATGACAGCGCGTCTTTGACAAGATGTT	801					
DB	721	CATAAAAT	CGCTGCCAGGATTTATGAAGAAATATGACAGCGCGTCTTTGACAAGATGTT	780					
QY	802	TCTAACT	ACTTAATCTCGGCTTTATCAGAGAAACCAAGCAGACATACACTGGAAGATGAA	861					
DB	781	TCTAACT	ACTTAATCTCGGCTTTATCAGAGAAACCAAGCAGACATACACTGGAAGATGAA	840					
QY	862	GTAGCAG	AGGTTTACAAAAATTAATCTCAAGGAGGCAACAAATATGAGGAGGATCCC	921					
DB	841	GTAGCAG	AGGTTTACAAAAATTAATCTCAAGGAGGCAACAAATATGAGGAGGATCCC	900					
QY	922	AATAAGCC	CACAAGCTGGACTGAGATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA	981					
DB	901	AATAAGCC	CACAAGCTGGACTGAGATCAGGCTGGAAAAATACCAGAGAAAGTGACTCCA	960					
QY	982	ATGGCAG	CAATTCAGATGGCTTCTGCTAAGGGAGAAAAAGATGAACAGATATCTAACACA	1041					
DB	961	ATGGCAG	CAATTCAGATGGCTTCTGCTAAGGGAGAAAAAGATGAACAGATATCTAACACA	1020					

QY	1042	TTAACTTG	CAAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTAGG	1101					
DB	1021	TTAACTTG	CAAAATGGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACCTTAGG	1080					
QY	1102	GACTTCC	CAATATTTCCCAAAATTTCTATGGCTACTGGAAGATTTGATTCAGAAAAAGAA	1161					
DB	1081	GAACTTCA	CAATATTTCCCAAAATTTCTATGGCTACTGGAAGATTTGATTCAGAAAAAGAA	1140					
QY	1162	GCAAAG	GAGAAAGAACACTGATTACTATCATGAAACACTGATTGACTTGTGAAGATG	1221					
DB	1141	GCAAAG	GAGAAAGAACACTGATTACTATCATGAAACACTGATTGACTTGTGAAGATG	1200					
QY	1222	ATGCTGA	AAATATGGAACCAATATCTCCAGAAAGGTGTTTCTACCTTGAAACCTTGGAT	1281					
DB	1201	ATGCTGA	AAATATGGAACCAATATCTCCAGAAAGGTGTTTCTACCTTGAAACCTTGGAT	1260					
QY	1282	GAAATG	ATTGCTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAAGC	1341					
DB	1261	GAAATG	ATTGCTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAAGC	1320					
QY	1342	AAAGCT	TTTCCAGCAGCAATCATGAGAAAGCTATGAAGAAACAGACAGTACCAGGAAGAA	1401					
DB	1321	AAAGCT	TTTCCAGCAGCAATCATGAGAAAGCTATGAAGAAACAGACAGTACCAGGAAGAA	1380					
QY	1402	CGAGCT	TAAGATGGAAGGAATATGGAAGCTTTGAAGGATTCACAAAAAGATGATACTCC	1461					
DB	1381	CGAGCT	TAAGATGGAAGGAATATGGAAGCTTTGAAGGATTCACAAAAAGATGATACTCC	1440					
QY	1462	AACCCAG	GAGAAAGACAGATGAACCCAAAGGAAACAGAGCCCTATTTGGAAGCCATC	1521					
DB	1441	AACCCAG	GAGAAAGACAGATGAACCCAAAGGAAACAGAGCCCTATTTGGAAGCCATC	1500					
QY	1522	ACAAAA	ATAATTTGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAAGATTATGAC	1581					
DB	1501	ACAAAA	ATAATTTGAATGGTTGAAGAAACATGACAAAAAGGAAATAAAGAAAGATTATGAC	1560					
QY	1582	CTTTCAA	AGATGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATC	1641					
DB	1561	CTTTCAA	AGATGAGACTTCATCAATAAACAGCTGATGCTTATGTGGAGAAAGGCATC	1620					
QY	1642	CTTGACA	AGGAAGACCCAGGCCATCAAGCCGATTTATAGAGCCCTGTAAAAATGGCAA	1701					
DB	1621	CTTGACA	AGGAAGACCCAGGCCATCAAGCCGATTTATAGAGCCCTGTAAAAATGGCAA	1680					
QY	1702	AAAGTCC	AGAGCTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACCTTCTAAT	1761					
DB	1681	AAAGTCC	AGAGCTTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACCTTCTAAT	1740					
QY	1762	TCGTGAT	TAAATTTTTTGACCCAGGGTTATTAGAAAGTGTCTGAATTTACAGTAGTTA	1821					
DB	1741	TCGTGAT	TAAATTTTTTGACCCAGGGTTATTAGAAAGTGTCTGAATTTACAGTAGTTA	1800					
QY	1822	ACCTTTT	ACAAGTGGTTAAAAACATAGCTTTCTCCCGTAAAAACATCTGGAAGTAAAGT	1881					
DB	1801	ACCTTTT	ACAAGTGGTTAAAAACATAGCTTTCTCCCGTAAAAACATCTGGAAGTAAAGT	1860					
QY	1882	TGATG	TAGCTGAGA	1897					
DB	1861	TGATG	TAGCTGAAA	1876					

RESULT 7
US-10-140-274-89
; Sequence 89, Application US/10140274
; Publication NO. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C161
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 89
LENGTH: 1893
TYPE: DNA
ORGANISM: Homo Sapien
US-10-140-274-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGCGTCACAGGAATTCAGCACCCACAGCGGCGGACAGCGCTCCCTCTACCTGGA 81
DB 1 GTCTCCGCGTCACAGGAATTCAGCACCCACAGCGGCGGACAGCGCTCCCTCTACCTGGA 60
QY 82 GACTTGACTCCCGCGGCGCCCAACCTTGCTTATCCCTTGACCGCTCGAGTGTGACAGATCC 141
DB 61 GACTTGACTCCCGCGGCGCCCAACCTTGCTTATCCCTTGACCGCTCGAGTGTGACAGATCC 120
QY 142 TGACGCGCGCCAGTCCCGCGCCCTCTCCGCGCCACACCCCTCTGCTGCTTCCCTGT 201
DB 121 TGACGCGCGCCAGTCCCGCGCCCTCTCCGCGCCACACCCCTCTGCTGCTTCCCTGT 180
QY 202 TTTTACTCTCTCTTTTCAATCAACAAAGCTTACAGCTCCAGAGGCCAGCGCCGGCT 261
DB 181 TTTTACTCTCTCTTTTCAATCAACAAAGCTTACAGCTCCAGAGGCCAGCGCCGGCT 240
QY 262 GTACCCCAAGCCGAGCGTGAAGATGGGGTTCCTCGGACCGGCACTTGGATTCGGTG 321
DB 241 GTACCCCAAGCCGAGCGTGAAGATGGGGTTCCTCGGACCGGCACTTGGATTCGGTG 300
QY 322 TTAGTGTCTCCGATTCAGCTTTCCCAACCTTGAGGAGGCCCAAGCAAAATCTCTACAT 381
DB 301 TTAGTGTCTCCGATTCAGCTTTCCCAACCTTGAGGAGGCCCAAGCAAAATCTCTACAT 360
QY 382 AATAGAGATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCGCTGAAGCAGAAAGAC 441
DB 361 AATAGAGATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCGCTGAAGCAGAAAGAC 420
QY 442 AAGATTAAGAAACATATCTCCAGAAACACAGCCAGGTCAGAGCACTATTCTTTGTT 501
DB 421 AAGATTAAGAAACATATCTCCAGAAACACAGCCAGGTCAGAGCACTATTCTTTGTT 480
QY 502 GATACTTGAACCTGTGAAGGCAATAACAGAAAGGAAATAATGAGAAAGAAAGACAA 561
DB 481 GATACTTGAACCTGTGAAGGCAATAACAGAAAGGAAATAATGAGAAAGAAAGACAA 540
QY 562 TCTATAAGAGCTCCCACTTGATATAAGTTGAATGTGAAGATGTTGATTCACCAAG 621
DB 541 TCTATAAGAGCTCCCACTTGATATAAGTTGAATGTGAAGATGTTGATTCACCAAG 600
QY 622 AATCGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 681
DB 601 AATCGAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 682 GATGATCCAGATGGTCTTTCATCACTAGACGGGACTCCCTTTAACCGCTGAAGACATTGTC 741

DB 661 GATGATCCAGATGCTCTTCACTAGAGGGGACTCCTTTAAGCGCTGAAGACATTGTC 720
QY 742 CATAAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTTGTTTGACAGATGTT 801
DB 721 CATAAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCCGTTGTTTGACAGATGTT 780
QY 802 TCTAAACTACTTAACTCTCGGCTTATCAGAAAGCCCAAGCAGATACACATGAGAGTAA 861
DB 781 TCTAAACTACTTAACTCTCGGCTTATCAGAAAGCCCAAGCAGATACACATGAGAGTAA 840
QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCCAAGCAGATGAGAGGATCCC 921
DB 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCCAAGCAGATGAGAGGATCCC 900
QY 922 AATAAGCCCAAGCTGGAGTGAATCAGGCTGGAAAAATACCAGAGAAAGTGAATCCA 981
DB 901 AATAAGCCCAAGCTGGAGTGAATCAGGCTGGAAAAATACCAGAGAAAGTGAATCCA 960
QY 982 ATGCGAGCAATTCAGATGGTCTTGTAGGGAGAAACAGTGAACAGTATCTAACACA 1041
DB 961 ATGCGAGCAATTCAGATGGTCTTGTAGGGAGAAACAGTGAACAGTATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAAACCTTACAGTGAAGACAACTTTAGG 1101
DB 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAAACCTTACAGTGAAGACAACTTTAGG 1080
QY 1102 GACTTCCAATATTTCCCAATTTCTATGGCTACTGAAAGTATTTGATTCAGAAAAAGAA 1161
DB 1081 GAACTCCAATATTTCCCAATTTCTATGGCTACTGAAAGTATTTGATTCAGAAAAAGAA 1140
QY 1162 GCAAAAGAGAAAGAAACACTGATTACTATCATGAAAGCACTGATTCACCTTTGTAAGATG 1221
DB 1141 GCAAAAGAGAAAGAAACACTGATTACTATCATGAAAGCACTGATTCACCTTTGTAAGATG 1200
QY 1222 ATGGTGAATATGGAACAATATCTCAGAAAGAGTGTGTTTCTTACCTTGAAGATTTGAT 1281
DB 1201 ATGGTGAATATGGAACAATATCTCAGAAAGAGTGTGTTTCTTACCTTGAAGATTTGAT 1260
QY 1282 GAAATGATTTGCTTTCAGACCAACAAAGCTAGAAAAAATGCTACTGACATATTAAGC 1341
DB 1261 GAAATGATTTGCTTTCAGACCAACAAAGCTAGAAAAAATGCTACTGACATATTAAGC 1320
QY 1342 AAGCTTTTCCAGCACCATTAGAGAGAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA 1401
DB 1321 AAGCTTTTCCAGCACCATTAGAGAGAGTCTATGAAGAAACAGACAGTACCAAGGAAGAA 1380
QY 1402 GCAGCTAAGATGGAAGAAATATGGAAGCTTGAAGGATTTCCACAAAAGATGATTAATCC 1461
DB 1381 GCAGCTAAGATGGAAGAAATATGGAAGCTTGAAGGATTTCCACAAAAGATGATTAATCC 1440
QY 1462 AACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAGCAAGCCCTATTGGAAGCCATC 1521
DB 1441 AACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAGCAAGCCCTATTGGAAGCCATC 1500
QY 1522 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGGAAATTAAGAGATTTATGAC 1581
DB 1501 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGGAAATTAAGAGATTTATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTCAATCAATCAAGCTGATGCTTATGTTGGAGAAAGGCATC 1641
DB 1561 CTTTCAAGATGAGAGACTTCAATCAATCAAGCTGATGCTTATGTTGGAGAAAGGCATC 1620
QY 1642 CTTTCAAGAGGAAAGCCGAGGCCATCAAGCCATTTATAGCAGCTGTAAAAATGGCAA 1701
DB 1621 CTTGACAGGAAAGCCGAGGCCATCAAGCCATTTATAGCAGCTGTAAAAATGGCAA 1680
QY 1702 AAGATCCAGGAGCTTTTCAACTGTTTCAAGAAACATAATATAGCTTTAAACACTTTCTAT 1761
DB 1681 AAGATCCAGGAGCTTTTCAACTGTTTCAAGAAACATAATATAGCTTTAAACACTTTCTAT 1740
QY 1762 TCTGTGATTAATAATTTTGTACCCCAAGGTTTATTAAGAAAGTCTCAATTTACAGTAGTTA 1821

Db 1741 TCTGTGATATAATTTTGTGACCCAGGGTTATTAGAAAGTCTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAAGTGTAAAAACATAGCTTTCTTCCCGTAAAAAAGTCTGAAAGTAAAGT 1881
Db 1801 ACCTTTACAAGTGTAAAAACATAGCTTTCTTCCCGTAAAAAAGTCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 8

US-10-140-471-89

; Sequence 89, Application US/10140471

; Publication No. US2003013887A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C163

; CURRENT APPLICATION NUMBER: US/10/140,471

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 89

; LENGTH: 1893

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-471-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGGTCCACAGGAATTCAGCACCCAGGGCGGACAGCGCTCCCTCTACCTGGA 81
Db 1 GTCTCCGGTCCACAGGAATTCAGCACCCAGGGCGGACAGCGCTCCCTCTACCTGGA 60
QY 82 GACTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGTACAGATCC 141
Db 61 GACTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGATCC 120
QY 142 TGCAGCCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGATCC 201
Db 121 TGCAGCCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTGCTTATCCCTTGACCGTGCAGATCC 180
QY 202 TTTTACTCTCTCTTTTCAATTAACAAAAGCTACAGCTCCAGGAGCCAGCGCGGGCT 261
Db 181 TTTTACTCTCTCTTTTCAATTAACAAAAGCTACAGCTCCAGGAGCCAGCGCGGGCT 240
QY 262 GTGACCCCAAGCCGAGCGGTGGAAGATGGGGTTCCTCGGACCCGCGACCTTGGATTCTGGTG 321
Db 241 GTGACCCCAAGCCGAGCGGTGGAAGATGGGGTTCCTCGGACCCGCGACCTTGGATTCTGGTG 300
QY 322 TTAGTGCTCCCGATTCAAGCTTTCCCAAAAGCTGGAGGAAGCCAGCAAAATCTCTACAT 381
Db 301 TTAGTGCTCCCGATTCAAGCTTTCCCAAAAGCTGGAGGAAGCCAGCAAAATCTCTACAT 360

QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATGCTGGAAGCAGAAGAAC 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTTGAATGAACAGATGCTGGAAGCAGAAGAAC 420
QY 442 AAGATTAATAAACAATATCTCCCAAAACAAGCCAGGTCAGAGCAACTATTTCTTTGTT 501
Db 421 AAGATTAATAAACAATATCTCCCAAAACAAGCCAGGTCAGAGCAACTATTTCTTTGTT 480
QY 502 GATAACTTTGAACCTGCTAAGGGCAATAACAGAAAAAGGAAAAAATTTGAGAAAAAGACAA 561
Db 481 GATAACTTTGAACCTGCTAAGGGCAATAACAGAAAAAGGAAAAAATTTGAGAAAAAGACAA 540
QY 562 TCTATPAGAAGCTCCCCACTTTGATATAAGTTGGAAGATGTTGATTCACCAAG 621
Db 541 TCTATPAGAAGCTCCCCACTTTGATATAAGTTGGAAGATGTTGATTCACCAAG 600
QY 622 AATCGAAAACCTGATCGATGATTTATGACTCTACTAAGAGTGGATTTGGATCATAAATTCNA 581
Db 601 AATCGAAAACCTGATCGATGATTTATGACTCTACTAAGAGTGGATTTGGATCATAAATTCNA 660
QY 682 GATGATCCAGATGCTTTCATCACTAGACGGGACTCTCTTAAACCGCTGAACACATGTC 741
Db 661 GATGATCCAGATGCTTTCATCACTAGACGGGACTCTCTTAAACCGCTGAACACATGTC 720
QY 742 CATAAATCGCTGCCAGGATTTTATGAAGAAAAATGACAGAGCGCTGTTTGACAAAGATGTT 801
Db 721 CATAAATCGCTGCCAGGATTTTATGAAGAAAAATGACAGAGCGCTGTTTGACAAAGATGTT 780
QY 802 TCTAAACTACTTAATCTCGGCTTATACAGAAAGCCAGACATACACTGGAAGATGAA 861
Db 781 TCTAAACTACTTAATCTCGGCTTATACAGAAAGCCAGACATACACTGGAAGATGAA 840
QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCAAATATATGAGGAGGATCCC 921
Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGGAGCCAAATATATGAGGAGGATCCC 900
QY 922 AATAAGCCCAACAGCTGGACTGAGATCAGGCTGGAAGAAATACAGAGAAAGTGTCTCA 981
Db 901 AATAAGCCCAACAGCTGGACTGAGATCAGGCTGGAAGAAATACAGAGAAAGTGTCTCA 960
QY 982 ATGGCAGCAATTCAGAGATGGTCTTCTAAGGGAGAAACAGATGAACAGATATCTAACACA 1041
Db 961 ATGGCAGCAATTCAGAGATGGTCTTCTAAGGGAGAAACAGATGAACAGATATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGGCTTGAAGAGGAGAACTAAACCTACAGTGAAGCAACTTTAGG 1101
Db 1021 TTAACCTTGACAAATGGCTTGAAGAGGAGAACTAAACCTACAGTGAAGCAACTTTAGG 1080
QY 1102 GACTTCCCAATATTTCCCAAAATTTCTATCGCTTACTGAAAAGTATTGATTTCAGAAAAAGAA 1161
Db 1081 GACTTCCCAATATTTCCCAAAATTTCTATCGCTTACTGAAAAGTATTGATTTCAGAAAAAGAA 1140
QY 1162 GCAAAAGAGAAAGAAACACTGATTTACTATCATGATGAAAACACTGATTTGCTGAAGATG 1221
Db 1141 GCAAAAGAGAAAGAAACACTGATTTACTATCATGATGAAAACACTGATTTGCTGAAGATG 1200
QY 1222 ATGTGTAATATGGAACAATATCTCCAGAGAGGCTTTCCCTACCTTGAACACTTTGGAT 1281
Db 1201 ATGTGTAATATGGAACAATATCTCCAGAGAAAGGCTTTCCCTACCTTGAACACTTTGGAT 1260
QY 1282 GAAATGATGCTTCTTCAGACCAAAAACAGCTAGAAAAAATGCTACTGACATATTAAGC 1341
Db 1261 GAAATGATGCTTCTTCAGACCAAAAACAGCTAGAAAAAATGCTACTGACATATTAAGC 1320
QY 1342 AAGCTTTTCCAGCACCATCATGAGAAAGATCATGAAGAAACAGACAGTACCAAGAGAA 1401
Db 1321 AAGCTTTTCCAGCACCATCATGAGAAAGATCATGAAGAAACAGACAGTACCAAGAGAA 1380
QY 1402 GCAGCTAAGATGGAAGAAAGAAATATGGAAGCTTTGAAGGATTTCCACAAAAGATGATAACTCC 1461
Db 1381 GCAGCTAAGATGGAAGAAAGAAATATGGAAGCTTTGAAGGATTTCCACAAAAGATGATAACTCC 1440

QY 1462 AACCCAGGAGGAAAGACAGATGAACCCAAAGAAAAACAGAAAGCCTATTGGAAGCCATC 1521
DB 1441 AACCCAGGAGGAAAGACAGATGAACCCAAAGAAAAACAGAAAGCCTATTGGAAGCCATC 1500
QY 1522 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAGATTATGAC 1581
DB 1501 AGAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATAAAGAGATTATGAC 1560
QY 1582 CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGCCATC 1641
DB 1561 CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGCCATC 1620
QY 1642 CTTGACAGGAGGAGCCGAGGCCATCAAGCGCATTTATAGACGCTGTAAAAATGGCAA 1701
DB 1621 CTTGACAGGAGGAGCCGAGGCCATCAAGCGCATTTATAGACGCTGTAAAAATGGCAA 1680
QY 1702 AAGATCCAGGAGCTTTCAACTGTTTCAGAAACATATATAGCTTAAACACACTTCTAAT 1761
DB 1681 AAGATCCAGGAGCTTTCAACTGTTTCAGAAACATATATAGCTTAAACACACTTCTAAT 1740
QY 1762 TCTGTGATTAAAAATTTTTCACCCCAAGGGTTATTAGAAAGTGTGTAATTTACAGTAGTTA 1821
DB 1741 TCTGTGATTAAAAATTTTTCACCCCAAGGGTTATTAGAAAGTGTGTAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1881
DB 1801 ACCTTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
DB 1861 TGTATGTAAGCTGAAA 1876

RESULT 9

US-10-140-807-89
; Sequence 89, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; Prior Filing DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-807-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 22 GTCTCCGCGTCACAGAACTTCAGCACCCAGGCGGACAGCGCTCCCTCTACCTGGA 81

DB 1 GTCTCCGCGTCACAGAACTTCAGCACCCAGGCGGACAGCGCTCCCTCTACCTGGA 60
QY 82 GACTTGACTCCCGCGGCCCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGTGACAGATCC 141
DB 61 GACTTGACTCCCGCGGCCCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGTGACAGATCC 120
QY 142 TGACAGCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTCTCTGCTCTCTGCTCTTCTGT 201
DB 121 TGACAGCGCCAGTCCCGGCCCTCTCCCGCCCAACCCCTCTCTGCTCTCTGCTCTTCTGT 180
QY 202 TTTTACT 261
DB 181 TTTTACT 240
QY 262 GTACCCCAAGCCGAGCGTGAAGATGGGGTTCCTCGGGACCGGCACTTTGGATTCTGGTG 321
DB 241 GTACCCCAAGCCGAGCGTGAAGATGGGGTTCCTCGGGACCGGCACTTTGGATTCTGGTG 300
QY 322 TTAGTCTCCCGGATTCAAGCTTTCCCAACCTGGAGGAGCCCAAGCAATCTCTACAT 381
DB 301 TTAGTCTCCCGGATTCAAGCTTTCCCAACCTGGAGGAGCCCAAGCAATCTCTACAT 360
QY 382 AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAGAAGAC 441
DB 361 AATAGAGAATTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAGAAGAC 420
QY 442 AAGATTAAAAAACAATATCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 501
DB 421 AAGATTAAAAAACAATATCTCCAGAAAAACAGCCAGGTCAGAGCAACTATTCTTTTGT 480
QY 502 GATACTTCAACTGCTTAAGGGCAATAACAGAAAAAGAAAAATTCAGAAAAAGACAAA 561
DB 481 GATACTTCAACTGCTTAAGGGCAATAACAGAAAAAGAAAAATTCAGAAAAAGACAAA 540
QY 562 TCTATAAGAAAGCTCCCACTTTGATATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 621
DB 541 TCTATAAGAAAGCTCCCACTTTGATATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 600
QY 622 AATCGAAAACTGATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATTAATTTCAA 581
DB 601 AATCGAAAACTGATCGATGATTATGACTCTACTAAGAGTGGATTGGATCATTAATTTCAA 660
QY 682 GATGATCCAGATGGTCTTCATCAACTAGACGGGACTCTTTAAACCGCTGAAGACATTGTC 741
DB 661 GATGATCCAGATGGTCTTCATCAACTAGACGGGACTCTTTAAACCGCTGAAGACATTGTC 720
QY 742 CATATAAATCGCTGCCAGGATTTATGAAGAAATGACAGACCGCTGTTTGACAAAGATTGTT 801
DB 721 CATATAAATCGCTGCCAGGATTTATGAAGAAATGACAGACCGCTGTTTGACAAAGATTGTT 780
QY 802 TCTAAACTACTTTAATCTCGGCTTATCAGAAAAAGCAAGCAATACACTGGAAGATGAA 861
DB 781 TCTAAACTACTTTAATCTCGGCTTATCAGAAAAAGCAAGCAATACACTGGAAGATGAA 840
QY 862 GTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCAACAATTTATGAGGAGGATCCC 921
DB 841 GTAGCAGAGGTTTTACAAAAATTAATCTCAAAGGAAGCAACAATTTATGAGGAGGATCCC 900
QY 922 AATAGCCCAAGCTGAGATGAGATCAGGCTGGAAAAATACCGAGAGAAAGTGAAGTCCA 981
DB 901 AATAGCCCAAGCTGAGATGAGATCAGGCTGGAAAAATACCGAGAGAAAGTGAAGTCCA 960
QY 982 ATGGCAGCAATTCAGATGGTCTTGCCTAAGGAGAAAAACGATGAACAGTATCTAACACA 1041
DB 961 ATGGCAGCAATTCAGATGGTCTTGCCTAAGGAGAAAAACGATGAACAGTATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACTACAGTGAAGACAACTTTAGG 1101
DB 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACTACAGTGAAGACAACTTTAGG 1080
QY 1102 GACTTCCAAATATTTCCCAATTTCTATGCGGCTACTGAAAAGTATTGATTCAGAAAAAGAA 1161
DB 1080 GACTTCCAAATATTTCCCAATTTCTATGCGGCTACTGAAAAGTATTGATTCAGAAAAAGAA 1140

Db 1081 GAATCCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATATGATTTCAGAAAAAGAA 1140
 QY 1162 GCAAAAGAGAAGAAACACTGATTACTATCATGAAACACACACTGATTGACTTTGTGAAGATG 1221
 Db 1141 CCAAAAGAGAAGAAACACTGATTACTATCATGAAACACACTGATTGACTTTGTGAAGATG 1200
 QY 1222 ATGTGAAATATGGAACAATATCTCCAGAAAGGTGTTCTTACCTTTGAAAACTTGGAT 1281
 Db 1201 ATGTGAAATATGGAACAATATCTCCAGAAAGGTGTTCTTACCTTTGAAAACTTGGAT 1260
 QY 1282 GAATGATTGCTCTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAGC 1341
 Db 1261 GAAATGATTGCTCTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAGC 1320
 QY 1342 AAGCTTTTCCAGACCATCAGAGAAGTGCATGAAGAAACAGACAGTACCAGGAAGAA 1401
 Db 1321 AAGCTTTTCCAGACCATCAGAGAAGTGCATGAAGAAACAGACAGTACCAGGAAGAA 1380
 QY 1402 GCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCACAAAAAGATGATAACTCC 1461
 Db 1381 GCAGCTAAGATGGAAGGAATATGGAAGCTTGAAGGATTCACAAAAAGATGATAACTCC 1440
 QY 1462 AACCAGGAGAAAGACAGATGACCCAAAGGAAGAAACAGAGGCTATTTGGAAGCCATC 1521
 Db 1441 AACCAGGAGAAAGACAGATGACCCAAAGGAAGAAACAGAGGCTATTTGGAAGCCATC 1500
 QY 1522 AGAAAAATATGGAATGTTGAAGAAACATCACAAAAAGGGAATTAAGAAGATTATGAC 1581
 Db 1501 AGAAAAATATGGAATGTTGAAGAAACATCACAAAAAGGGAATTAAGAAGATTATGAC 1560
 QY 1582 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1641
 Db 1561 CTTTCAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC 1620
 QY 1642 CTTGACAGGAAGAGCGAGCCCATCAAGCGCATTTATAGCAGCTGTAATAATGGCAA 1701
 Db 1621 CTTGACAGGAAGAGCGAGCCCATCAAGCGCATTTATAGCAGCTGTAATAATGGCAA 1680
 QY 1702 AAGATCCAGGAGTCTTCAACTGTTTCAGAAAAACATATATAGCTTAAACACATTCATAAT 1761
 Db 1681 AAGATCCAGGAGTCTTCAACTGTTTCAGAAAAACATATATAGCTTAAACACATTCATAAT 1740
 QY 1762 TCTGTGATATAATTTTGTACCAAGGGTTATTAGAAAGTCTCAATTTACAGTAGTTA 1821
 Db 1741 TCTGTGATATAATTTTGTACCAAGGGTTATTAGAAAGTCTCAATTTACAGTAGTTA 1800
 QY 1822 ACCTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAAATCTATCTGAAAGTAAAGT 1881
 Db 1801 ACCTTTACAGTGGTTAAACATAGCTTTCTTCCCGTAAAAAATCTATCTGAAAGTAAAGT 1860
 QY 1882 TGTATGTAAGCTGAGA 1897
 Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 10

US-10-140-922-89
 ; Sequence 89, Application US/10140922

; Publication No. US2003013889A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Beresini, Maureen
 ; APPLICANT: DeForge, Laura
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Sherwood, Steven
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Collin K
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3330R1C179
 ; CURRENT APPLICATION NUMBER: US/10/140,922
 ; CURRENT FILING DATE: 2002-05-07
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 89
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-140-922-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGGTCCACAGGAATTCAGACCCACAGGCGGACAGCGCTCCCTCTACCTGGA 81
 Db 1 GTCTCCGGTCCACAGGAATTCAGACCCACAGGCGGACAGCGCTCCCTCTACCTGGA 60
 QY 82 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTTGACCGTGCAGTGTCCAGAGATCC 141
 Db 61 GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTTGACCGTGCAGTGTCCAGAGATCC 120
 QY 142 TGCAGCCCGCAGTCCCGCGCCCTCTCCCGCCCAACCCACCCCTCTCTGCTGTCTGT 201
 Db 121 TGCAGCCCGCAGTCCCGCGCCCTCTCCCGCCCAACCCACCCCTCTCTGCTGTCTGT 180
 QY 202 TTTTACTCTCTTTTCATTATACAAAAAGCTACAGCTCCAGGAGCCCGCGGCT 261
 Db 181 TTTTACTCTCTTTTCATTATACAAAAAGCTACAGCTCCAGGAGCCCGCGGCT 240
 QY 262 GTGACCCAAAGCGGAGCGTGGGAAGATGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG 321
 Db 241 GTGACCCAAAGCGGAGCGTGGGAAGATGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG 300
 QY 322 TTAGTGTCTCCGATTCAGCTTTCCCAACCTCGGAGGAGCAAAATCTCTACAT 381
 Db 301 TTAGTGTCTCCGATTCAGCTTTCCCAACCTCGGAGGAGCAAAATCTCTACAT 360
 QY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGATGAACAGATTTGCTGAAGCAGAAAGAC 441
 Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGATGAACAGATTTGCTGAAGCAGAAAGAC 420
 QY 442 AAGATTAAAAAACAATATCTCCGAAACCAAGCCAGGTCAGAGCAACTATTCTTTTGT 501
 Db 421 AAGATTAAAAAACAATATCTCCGAAACCAAGCCAGGTCAGAGCAACTATTCTTTTGT 480
 QY 502 GATACTTTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAAATTTGAGAAAGAAAGACAA 561
 Db 481 GATACTTTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAAATTTGAGAAAGAAAGACAA 540
 QY 562 TCTATAAGAGCTCCCGACCTTCATATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 621
 Db 541 TCTATAAGAGCTCCCGACCTTCATATAAGTTGAATGTGAAGATGTTGATTCAACCAAG 600
 QY 622 AATCGAAACTGATCGATGATTGACTCTACTAAGAGTGGATTGGATTCATAAATTTCAA 681
 Db 601 AATCGAAACTGATCGATGATTGACTCTACTAAGAGTGGATTGGATTCATAAATTTCAA 660
 QY 682 GATGATCCAGATGTTCTTCATCAACTAGACGGGACTCCTTTAACCGCTGAAGACATGTC 741
 Db 661 GATGATCCAGATGTTCTTCATCAACTAGACGGGACTCCTTTAACCGCTGAAGACATGTC 720
 QY 742 CATAAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCGGCTGTTTGACAGAGATTGT 801
 Db 721 CATAAAATCGCTGCCAGGATTTATGAAGAAATGACAGAGCGGCTGTTTGACAGAGATTGT 780

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QY 802 TCTAACTACTTAATCTCGGCTTATCACGAAAGCCACATACACTGGAAGATGAA 861
Db 781 TCTAACTACTTAATCTCGGCTTATCACGAAAGCCACATACACTGGAAGATGAA 840
QY 852 GTACGAGAGTTTACAAAATTAATCTCAAGGAAGCCACAAATATTAGGAGATCCC 921
Db 841 GTACGAGAGTTTACAAAATTAATCTCAAGGAAGCCACAAATATTAGGAGATCCC 900
QY 922 AATAAGCCCAAGCTGGACTGAGAAATCAGGCTGGAATAATACCAGAGAAAGTCACTCCA 981
Db 901 AATAAGCCCAAGCTGGACTGAGAAATCAGGCTGGAATAATACCAGAGAAAGTCACTCCA 960
QY 982 ATGCGACAAATTCAGATGGCTTCTCAAGGAGAAACAGATGAACAGTATCTAACACA 1041
Db 961 ATGCGACAAATTCAGATGGCTTCTCAAGGAGAAACAGATGAACAGTATCTAACACA 1020
QY 1042 TTAACCTTGCAAAATGCTTGGAAAGGAGAACTAAAACCTACAGTGAAGCAACTTTAGG 1101
Db 1021 TTAACCTTGCAAAATGCTTGGAAAGGAGAACTAAAACCTACAGTGAAGCAACTTTAGG 1080
QY 1102 GACTTCCAAATATTCCCAATTTCTATCGCTACTGAAAAAGTATTGATTCAGAAAAAGAA 1161
Db 1081 GAATCCAAATATTCCCAATTTCTATCGCTACTGAAAAAGTATTGATTCAGAAAAAGAA 1140
QY 1162 GCRAAGAGAAAGAAACACTGATTACTATCATGAARACACTGATTGCTTTGAGATG 1221
Db 1141 GCRAAGAGAAAGAAACACTGATTACTATCATGAARACACTGATTGCTTTGAGATG 1200
QY 1222 ATGCTGAATATGAAACAAATATCTCCAGAAAGGTGTTTCCCTACCTTGAACACTTGGAT 1281
Db 1201 ATGCTGAATATGAAACAAATATCTCCAGAAAGGTGTTTCCCTACCTTGAACACTTGGAT 1260
QY 1282 GAATGATGCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC 1341
Db 1261 GAATGATGCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC 1320
QY 1342 AAGCTTTTCCAGCACCATCAGAGAAAGATCATGAGAAACACAGACAGTACCAGGAAGAA 1401
Db 1321 AAGCTTTTCCAGCACCATCAGAGAAAGATCATGAGAAACACAGACAGTACCAGGAAGAA 1380
QY 1402 GCAGCTAAGATGAAAGGAATATGGAAGCTTCAAGGATTCACAAAGATGATAACTCC 1461
Db 1381 GCAGCTAAGATGAAAGGAATATGGAAGCTTCAAGGATTCACAAAGATGATAACTCC 1440
QY 1462 AACCCAGGAGAAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATC 1521
Db 1441 AACCCAGGAGAAAGACAGATGAACCCAAAGGAAAAACAGAGCCCTATTGGAAGCCATC 1500
QY 1522 AGAAAAATATTGAATGGTTGAGAAACATGACAAAAAGGGAATTAAGAGATTTATGAC 1581
Db 1501 AGAAAAATATTGAATGGTTGAGAAACATGACAAAAAGGGAATTAAGAGATTTATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGAGAGAAAGGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTCATCAATAAACAGCTGATGCTTATGAGAGAAAGGCATC 1620
QY 1642 CTTGACAAAGAGAACCCGAGGCCATCAAGCGCATTTATAGAGCGCTGTAAATAATGGCAA 1701
Db 1621 CTTGACAAAGAGAACCCGAGGCCATCAAGCGCATTTATAGAGCGCTGTAAATAATGGCAA 1680
QY 1702 AAGATCCAGAGTCTTTCAACTGTTTTCAGAAACATATATAGCTTAACACTTCTAAT 1761
Db 1681 AAGATCCAGAGTCTTTCAACTGTTTTCAGAAACATATATAGCTTAACACTTCTAAT 1740
QY 1762 TCTGTGATTAATTTTTTGACCCCAAGGCTTATTAGAAAGTCTGAAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATTTTTTGACCCCAAGGCTTATTAGAAAGTCTGAAATTTACAGTAGTTA 1800
QY 1822 ACCTTTCAAGTGTATAAATAGCTTTCTCCGTTAAACATCTCTGAAAGTAAAGT 1881
Db 1801 ACCTTTCAAGTGTATAAATAGCTTTCTCCGTTAAACATCTCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
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Db 1861 TGTATGTAAGCTGAAA 1876
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RESULT 11

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US-10-140-924-89
; Sequence 89, Application US/10140924
; Publication No. US20030134355A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C177
; CURRENT APPLICATION NUMBER: US/10/140, 924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-924-89
```

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 22 GTCTCGCTCACAGGAACCTTCAGCACCCACAGCGCGGACAGCGCTCCCTCTTACCTGGA 81
Db 1 GTCTCGCTCACAGGAACCTTCAGCACCCACAGCGCGGACAGCGCTCCCTCTTACCTGGA 60
QY 82 GACTTGACTCCCGCGGCGCCCAACCTGCTTTATCCCTTGACCGTGCAGTGTGAGAGATCC 141
Db 61 GACTTGACTCCCGCGGCGCCCAACCTGCTTTATCCCTTGACCGTGCAGTGTGAGAGATCC 120
QY 142 TCGAGCGGCCAGTCCCGGCGCTCTCCCGCCCAACACCCACCGCTCCCTGGCTTCTCTGT 201
Db 121 TCGAGCGGCCAGTCCCGGCGCTCTCCCGCCCAACACCCACCGCTCCCTGGCTTCTCTGT 180
QY 202 TTTTACTCTCTCTTTTTCATTTCAATAAAGCTACAGCTTCCAGAGCCAGCGCGCGGCT 261
Db 181 TTTTACTCTCTCTTTTTCATTTCAATAAAGCTACAGCTTCCAGAGCCAGCGCGCGGCT 240
QY 262 GTGACCCCAAGCGCGGTGGGAAGATGGGTTCTTCGGGACCGGCACTTGGATTCTGGTG 321
Db 241 GTGACCCCAAGCGCGGTGGGAAGATGGGTTCTTCGGGACCGGCACTTGGATTCTGGTG 300
QY 322 TTAGTGCCTCCCGATTTCAAGCTTTCCCAAACTGGAGGAAGCAAGACAAATCTCTACAT 381
Db 301 TTAGTGCCTCCCGATTTCAAGCTTTCCCAAACTGGAGGAAGCAAGACAAATCTCTACAT 360
QY 382 AATAGAGAAATTAAGTGCAGAAAGACTTTTGAATGAACAGATTTGCTGAAGCAAGAAAGAC 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACTTTTGAATGAACAGATTTGCTGAAGCAAGAAAGAC 420
QY 442 AAGATTAATAAATAATATCTCCAGAAACAGCGCTTCAGAGCAACTATCTTTTGT 501
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142 TGCAGCCGCGCAGTCCCGGGCCCTCTCCCGCCCCACACCCACCCTCTCGCTTCCTGT 201
121 TGCAGCCGCGCAGTCCCGGGCCCTCTCCCGCCCCACACCCACCCTCTCGCTTCCTGT 180
202 TTTTACTCCCTCTTTTCATATCAATAACAAAGCTACAGCTCCAGAGCCGCGCGGGCT 261
181 TTTTACTCCCTCTTTTCATATCAATAACAAAGCTACAGCTCCAGAGCCGCGCGGGCT 240
262 GTGACCCAAAGCCGAGCTGGAAGAAATGGGGTTCCTCGGGACCGGCACTTGGATTCTCGTG 321
241 GTGACCCAAAGCCGAGCTGGAAGAAATGGGGTTCCTCGGGACCGGCACTTGGATTCTCGTG 300
322 TTAGTGCTCCGATTCAGCTTTCCCAAACCTGGAGGAAGCCAAAGCAAAATCTCTACAT 381
301 TTAGTGCTCCGATTCAGCTTTCCCAAACCTGGAGGAAGCCAAAGCAAAATCTCTACAT 360
382 AATAGAGAAATTAAGTCAGAAAGACCTTTTCAATGAACAGATTGCTGAAGCAGAAAGAC 441
361 AATAGAGAAATTAAGTCAGAAAGACCTTTTCAATGAACAGATTGCTGAAGCAGAAAGAC 420
442 AAGATTAAAAAACAATATCTCCAGAAACAAGCCAGGTCAGAGCAACTATCTTTTGGT 501
421 AAGATTAAAAAACAATATCTCCAGAAACAAGCCAGGTCAGAGCAACTATCTTTTGGT 480
502 GATAACTTGAACCTGCTTAAGGGCAATACAGAAAGGAAAAATTTGAGAAAGAAAGACAA 561
481 GATAACTTGAACCTGCTTAAGGGCAATACAGAAAGGAAAAATTTGAGAAAGAAAGACAA 540
562 TCTATAGAAGCTCCCACTTGATATGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 621
541 TCTATAGAAGCTCCCACTTGATATGAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGA 600
622 AATCGAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTGGATCATAAATTTCAA 681
601 AATCGAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTGGATCATAAATTTCAA 660
682 GATGATCCAGATGGCTTTCATCACTAGAGGGGACTCCTTTAACCGCTGAAGACATGTC 741
661 GATGATCCAGATGGCTTTCATCACTAGAGGGGACTCCTTTAACCGCTGAAGACATGTC 720
742 CATAAATCGCTCCAGGATTTATGAAGAAATGACAGAGCCGCTGTTTGACAGATTGTT 801
721 CATAAATCGCTCCAGGATTTATGAAGAAATGACAGAGCCGCTGTTTGACAGATTGTT 780
802 TCTAAACTACTTAATCTCGGCTTTATCAGAAAGCCAGCAATACACTGGAAGATGAA 861
781 TCTAAACTACTTAATCTCGGCTTTATCAGAAAGCCAGCAATACACTGGAAGATGAA 840
862 GTAGCAGAGTGTTCACAAAATTAATCTCAAGGAAGCCCAACAAATATGAGGAGATCCC 921
841 GTAGCAGAGTGTTCACAAAATTAATCTCAAGGAAGCCCAACAAATATGAGGAGATCCC 900
922 AATAAGCCCAAGCTGGACTGAGATCAGGCTGGAAAAATACCAGAGAAAGTGAATCCA 981
901 AATAAGCCCAAGCTGGACTGAGATCAGGCTGGAAAAATACCAGAGAAAGTGAATCCA 960
982 ATGGCAGCAATTCAGATGGCTTGTCTAAGGGAGAAAAACGATGAACATATCTTAACACA 1041
961 ATGGCAGCAATTCAGATGGCTTGTCTAAGGGAGAAAAACGATGAACATATCTTAACACA 1020
1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACTACAGTGAACACAACTTAGG 1101
1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTAAAACTACAGTGAACACAACTTAGG 1080
1102 GACTTCCAATATTTCCAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAGAA 1161
1081 GAATCCAATATTTCCAAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAGAA 1140
1162 GCAAGAGCAAGAAACACTGATTACTATCATGAACAACTGATTGACTTTGTGAAGATG 1221
1141 GCAAGAGCAAGAAACACTGATTACTATCATGAACAACTGATTGACTTTGTGAAGATG 1200
1222 ATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACTCTTGAACAACTTGGAT 1281

1201 ATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACTCTTGAACACTTGGAT 1260
1282 GAATGATGCTCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAGC 1341
1261 GAATGATGCTCTTTCAGACCAAAACAAAGCTAGAAAAAATGCTACTGCAATATAGC 1320
1342 AAGCTTTTCCAGCACCATCAGAGAGAGTCATGAACAAACAGACACTACCAAGGAAGAA 1401
1321 AAGCTTTTCCAGCACCATCAGAGAGAGTCATGAAGAAACAGACACTACCAAGGAAGAA 1380
1402 GCAGCTAAGATGGAAGAGGAATATGGAAGCTTGAAGGATTTCCACAAAAGATGATACTCC 1461
1381 GCAGCTAAGATGGAAGAGGAATATGGAAGCTTGAAGGATTTCCACAAAAGATGATACTCC 1440
1462 AACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAGCCTATTTGGAGGCCATC 1521
1441 AACCCAGGAGGAAGACAGATGAACCCAAAGGAAAAACAGAGCCTATTTGGAGGCCATC 1500
1522 AGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATTAAGAGATTATGAC 1581
1501 AGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAAGGGAATTAAGAGATTATGAC 1560
1582 CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTTATGTGGAAGAGGCATC 1641
1561 CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTTATGTGGAAGAGGCATC 1620
1642 CTTGACAAAGGAAGCCGAGGCCATCAAGCGGATTTATAGAGCCTGTAAAAATGGCAA 1701
1621 CTTGACAAAGGAAGCCGAGGCCATCAAGCGGATTTATAGAGCCTGTAAAAATGGCAA 1680
1702 AAGATCCAGGAGTCTTTCAACTCTTTCAGAAAAACATAATAGCTTAAAAACACTTCTAAT 1761
1681 AAGATCCAGGAGTCTTTCAACTCTTTCAGAAAAACATAATAGCTTAAAAACACTTCTAAT 1740
1762 TCTGTGATTAATAATTTTGGACCAAGGGTATTAGAAAAGTGTGTAATTTACAGTAGTTA 1821
1741 TCTGTGATTAATAATTTTGGACCAAGGGTATTAGAAAAGTGTGTAATTTACAGTAGTTA 1800
1822 ACCTTTTACAAGTGGTTAAACATAGCTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1881
1801 ACCTTTTACAAGTGGTTAAACATAGCTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT 1860
1882 TGTATGTAAGCTGAGA 1897
1861 TGTATGTAAGCTGAAA 1876

RESULT 13

US-10-141-698-89
; Sequence 89, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C206

; CURRENT APPLICATION NUMBER: US/10/141.698
 ; CURRENT FILING DATE: 2002-05-08
 ; Prior Application removed - See Palm or File Wrapper
 ; NUMBER OF SEQ ID NOS: 550
 ; SEQ ID NO 89
 ; LENGTH: 1893
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-141-698-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	22	GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGCGCGACAGCGCTCCCTCTACCTGGA	81
Db	1	GTCTCCGCGTCACAGGAACCTTCAGCACCCACAGCGCGACAGCGCTCCCTCTACCTGGA	60
Qy	82	GACTTTGACTCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGCTCGAGTGTGAGATCC	141
Db	61	GACTTGACTCCGCGCGCCCAACCCCTGCTTATCCCTTGACCGCTCGAGTGTGAGATCC	120
Qy	142	TGCAGCGCGCGAGTCCCGGCGCCCTCTCCGCGCCACACACCCCTCTCTCTCTCTCTCT	201
Db	121	TGCAGCGCGCGAGTCCCGGCGCCCTCTCTCCGCGCCACACACCCCTCTCTCTCTCTCT	180
Qy	202	TTTTTACT	261
Db	181	TTTTTACT	240
Qy	262	GTGACCCCAAGCGGCGTGGGAAGTGGGGTTCCTCGGCGCGCGCGCGCGCGCGCGCT	321
Db	241	GTGACCCCAAGCGGCGTGGGAAGTGGGGTTCCTCGGCGCGCGCGCGCGCGCGCGCT	300
Qy	322	TTAGTGTCTCCGATTCAGCTTTCCCAACCTCGGAGGAGCCAGCAATCTCTACAT	381
Db	301	TTAGTGTCTCCGATTCAGCTTTCCCAACCTCGGAGGAGCCAGCAATCTCTACAT	360
Qy	382	AATAGAGAAATTAAGTCAGAGAAAGACCTTTGAATGAACAGATTTGCTGAAGCAGAGAAGAC	441
Db	361	AATAGAGAAATTAAGTCAGAGAAAGACCTTTGAATGAACAGATTTGCTGAAGCAGAGAAGAC	420
Qy	442	AAGATTAAAAAACAATATCTCCAGAAACAGCCAGGTTCAGAGCAACTATCTTTTGT	501
Db	421	AAGATTAAAAAACAATATCTCCAGAAACAGCCAGGTTCAGAGCAACTATCTTTTGT	480
Qy	502	GATTAAGAGCTCCCGCTTGAAGGCAATACAGAAAGGAAAGAAATTTGAGAAAGACAA	561
Db	481	GATTAAGAGCTCCCGCTTGAAGGCAATACAGAAAGGAAAGAAATTTGAGAAAGACAA	540
Qy	562	TCTATAAGAGCTCCCGCTTGAAGGCAATACAGAAAGGAAAGAAATTTGAGAAAGACAA	621
Db	541	TCTATAAGAGCTCCCGCTTGAAGGCAATACAGAAAGGAAAGAAATTTGAGAAAGACAA	600
Qy	622	AATCGAAACTGATCGATGATTAAGTCTACTAAGAGTGGATGGATCAATAATTTCAA	681
Db	601	AATCGAAACTGATCGATGATTAAGTCTACTAAGAGTGGATGGATCAATAATTTCAA	660
Qy	682	GATGATCCAGATGGTCTTCACTAAGAGTGGATGGATGGATGGATGGATGGATGGAT	741
Db	661	GATGATCCAGATGGTCTTCACTAAGAGTGGATGGATGGATGGATGGATGGATGGAT	720
Qy	742	CATTAAGATCGTCCGAGATTTATGAAGAAATGACAGAGCGGTGTTGACAGATTTGT	801
Db	721	CATTAAGATCGTCCGAGATTTATGAAGAAATGACAGAGCGGTGTTGACAGATTTGT	780
Qy	802	TCTAAACTACTTAACTTCGGCTTATCAGAGAAAGCCAGCAGACATACCTGGAGATGAA	861
Db	781	TCTAAACTACTTAACTTCGGCTTATCAGAGAAAGCCAGCAGACATACCTGGAGATGAA	840
Qy	862	GTAGCAGAGGTTTTTACAAAAATTAATCTCAAGAGGAGCCCAACAAATTTAGAGGATGCC	921
Db	841	GTAGCAGAGGTTTTTACAAAAATTAATCTCAAGAGGAGCCCAACAAATTTAGAGGATGCC	900

Qy	922	AATAAGCCCAACAGCTGGACTGAGATCAGGCTGGAAAAATACAGAGAAAGTGAAGTCA	981
Db	901	AATAAGCCCAACAGCTGGACTGAGATCAGGCTGGAAAAATACAGAGAAAGTGAAGTCA	960
Qy	982	ATGCAGCAATTCAGATGCTGCTTGTCTAAGGAGAAAAACGATGAACAGTATCTAAACACA	1041
Db	961	ATGCAGCAATTCAGATGCTGCTTGTCTAAGGAGAAAAACGATGAACAGTATCTAAACACA	1020
Qy	1042	TTAACCCTGACAAATGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACTTTAGG	1101
Db	1021	TTAACCCTGACAAATGCTTGGAAAGGAGAACTAAACCTACAGTGAAGACAACTTTAGG	1080
Qy	1102	GACTTCCAATATTTCCCAAAATTTCTATCGCGTACTGAAAGCTATTGATTCAGAAAAAGAA	1161
Db	1081	GACTTCCAATATTTCCCAAAATTTCTATCGCGTACTGAAAGCTATTGATTCAGAAAAAGAA	1140
Qy	1162	GCAAAGAGAAAGAAACACTGATTACTATCATGAAACACACTGATTGTTGTGAAGATG	1221
Db	1141	GCAAAGAGAAAGAAACACTGATTACTATCATGAAACACACTGATTGTTGTGAAGATG	1200
Qy	1222	ATGCTGAATATGAAACAAATATCTCCAGAAAGGTGTTCTTACCTTGAACAACTTGGAT	1281
Db	1201	ATGCTGAATATGAAACAAATATCTCCAGAAAGGTGTTCTTACCTTGAACAACTTGGAT	1260
Qy	1282	GAAATGATTGCTTCTAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC	1341
Db	1261	GAAATGATTGCTTCTAGACCAAAACAAAGCTAGAAAAAATGCTACTGACAAATATAAGC	1320
Qy	1342	AAGCTTTTCCAGCACCACATCAGAGAAGAGTCTATGAAGAAACAGACAGTACCAGGAAGAA	1401
Db	1321	AAGCTTTTCCAGCACCACATCAGAGAAGAGTCTATGAAGAAACAGACAGTACCAGGAAGAA	1380
Qy	1402	GCAGCTAAGATGGAAGGAATATGGAAGCTTTGAAGGATTTCCACAAAAGATGATAACTCC	1461
Db	1381	GCAGCTAAGATGGAAGGAATATGGAAGCTTTGAAGGATTTCCACAAAAGATGATAACTCC	1440
Qy	1462	AACCCAGGAGGAGAGACAGATGAACCCAAAGAAAAACAGAGCCCTATTGGAAGCCATC	1521
Db	1441	AACCCAGGAGGAGAGACAGATGAACCCAAAGAAAAACAGAGCCCTATTGGAAGCCATC	1500
Qy	1522	AGAAAAAATATTGAATGTTGAAGAAACATGACAAAAAGGAAATTAAGAGATTTATGAC	1581
Db	1501	AGAAAAAATATTGAATGTTGAAGAAACATGACAAAAAGGAAATTAAGAGATTTATGAC	1560
Qy	1582	CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTTGGAGAAAGGATC	1641
Db	1561	CTTTCAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTTGGAGAAAGGATC	1620
Qy	1642	CTTCACAAAGGAGAGCGGAGCCATCAAGCGCATTTATAGCAGCTGTAATAATGGCAA	1701
Db	1621	CTTCACAAAGGAGAGCGGAGCCATCAAGCGCATTTATAGCAGCTGTAATAATGGCAA	1680
Qy	1702	AAGATCCAGGAGTCTTTCACTGTTTTCAGAAAAACATATATAGCTTAAACACATCTTAAT	1761
Db	1681	AAGATCCAGGAGTCTTTCACTGTTTTCAGAAAAACATATATAGCTTAAACACATCTTAAT	1740
Qy	1762	TCTGTGATTAATAATTTTGTGACCAAGGTTTATTAGAAAGTGTGAAATTTACAGTAGTTA	1821
Db	1741	TCTGTGATTAATAATTTTGTGACCAAGGTTTATTAGAAAGTGTGAAATTTACAGTAGTTA	1800
Qy	1822	ACCTTTTACAGTGGTTTAAACATAGCTTTCTCCCGTAAAAACATATCTGAAAGTAAAGT	1881
Db	1801	ACCTTTTACAGTGGTTTAAACATAGCTTTCTCCCGTAAAAACATATCTGAAAGTAAAGT	1860
Qy	1882	TGATGTAAGCTGAGA	1897
Db	1861	TGATGTAAGCTGAGA	1876

RESULT 14
 US-10-141-702-89
 ; Sequence 89, Application US/10141702

Publication No. US20030134358A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE OF INVENTION: ACIDS ENCODING THE SAME
 FILE REFERENCE: P3330R1C208
 CURRENT APPLICATION NUMBER: US/10/141,702
 CURRENT FILING DATE: 2002-05-08
 Prior Application removed - See Palm or File Wrapper
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO 89
 LENGTH: 1893
 TYPE: DNA
 ORGANISM: Homo Sapien
 US-10-141-702-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY	22	GTCTCCGCGTCACAGGAATTCAGACACACAGGGGGGACAGGCTCCCTCTACCTGGA	81
DB	1	GTCTCCGCGTCACAGGAATTCAGACACACAGGGGGGACAGGCTCCCTCTACCTGGA	60
QY	82	GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTGACGCTCGAGTGCAGAGATCC	141
DB	61	GACTTGACTCCCGCGCGCCCAACCTGCTTATCCCTTGACGCTCGAGTGCAGAGATCC	120
QY	142	TGCAGCGCGCGTCCCGCGCGCTTCGCCGCCACACCCCTCTCGCTCTTCCTGT	201
DB	121	TGCAGCGCGCGTCCCGCGCGCTTCGCCGCCACACCCCTCTCGCTCTTCCTGT	180
QY	202	TTTTACTCTCTCTTTTCATTCATACAAAGCTACAGCTCCAGGAGCCCGCGGGCT	261
DB	181	TTTTACTCTCTCTTTTCATTCATACAAAGCTACAGCTCCAGGAGCCCGCGGGCT	240
QY	262	GTGACCCAAAGCGAGCGTGAAGAATGGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	321
DB	241	GTGACCCAAAGCGAGCGTGAAGAATGGGGTTCCTCGGACCGGCACCTTGGATTCTGGTG	300
QY	322	TTAGTGCTCCGATTCAAGCTTTCCCAACCTGAGGAGGCCAAGACAAATCTCTACAT	381
DB	301	TTAGTGCTCCGATTCAAGCTTTCCCAACCTGAGGAGGCCAAGACAAATCTCTACAT	360
QY	382	AATAGAGATTAAAGTGCAGAAAGCTTTGAATGAACAGTTCGCTGAAGCAGAAAGAC	441
DB	361	AATAGAGATTAAAGTGCAGAAAGCTTTGAATGAACAGTTCGCTGAAGCAGAAAGAC	420
QY	442	AAGATTAATAAACATATCTCCAGAAACAGCGAGGTTCAGAGCAACTATCTTTTGT	501
DB	421	AAGATTAATAAACATATCTCCAGAAACAGCGAGGTTCAGAGCAACTATCTTTTGT	480
QY	502	GATACTTGAACCTCTTAGGCGCATACAGAAAAAGAAAAATTTGAGAAAAAGACAA	561
DB	481	GATACTTGAACCTCTTAGGCGCATACAGAAAAAGAAAAATTTGAGAAAAAGACAA	540
QY	562	TCATATAAGAGCTCCCACTTGATATAAGTTGAATGTGGAGATGTTGATTCACCAAG	621

DB	541	TCATATAAGAGCTCCCACTTGATATAAGTTGAATGTGGAGATGTTGATTCACCAAG	600
QY	622	AATCGAAAACCTGATCGATGATTTACTCTACTAAGAGTGGATGGATCATATAATTTCAA	681
DB	601	AATCGAAAACCTGATCGATGATTTACTCTACTAAGAGTGGATGGATCATATAATTTCAA	660
QY	682	GATGATCCAGATGCTTTCATCACTAGACGGGACCTTTAAACCCTGAAGCATTTGTC	741
DB	661	GATGATCCAGATGCTTTCATCACTAGACGGGACCTTTAAACCCTGAAGCATTTGTC	720
QY	742	CATAAAATCGCTCCAGGATTTATGAAGAAATTCACAGAGCCGCTGTTTGAACAAGTTGT	801
DB	721	CATAAAATCGCTCCAGGATTTATGAAGAAATTCACAGAGCCGCTGTTTGAACAAGTTGT	780
QY	802	TCATAACTACTTAACTCGGCCCTTATCAGAAAGCCCAAGCATACACTGGAAGATGAA	861
DB	781	TCATAACTACTTAACTCGGCCCTTATCAGAAAGCCCAAGCATACACTGGAAGATGAA	840
QY	862	GTAGCAGAGCTTTTACAAAAATTAATCTCAAAAGGAAGCCCAACAAATTTATGAGGAGTCC	921
DB	841	GTAGCAGAGCTTTTACAAAAATTAATCTCAAAAGGAAGCCCAACAAATTTATGAGGAGTCC	900
QY	922	AATAAGCCCAAGCTGGACTGAGAAATCAGGCTGGAATAATACAGAGAAAGTGAATCTCA	981
DB	901	AATAAGCCCAAGCTGGACTGAGAAATCAGGCTGGAATAATACAGAGAAAGTGAATCTCA	960
QY	982	ATGGCAGCAATTCAGATGCTTGTCTAAGGGAGAAACAGATGTAACACATCTTAACACA	1041
DB	961	ATGGCAGCAATTCAGATGCTTGTCTAAGGGAGAAACAGATGTAACACATCTTAACACA	1020
QY	1042	TTAACTCTGACAAATGGCTTGGAAAGGAGAACTTAAACCTTACAGTGAAGACAACTTTAGG	1101
DB	1021	TTAACTCTGACAAATGGCTTGGAAAGGAGAACTTAAACCTTACAGTGAAGACAACTTTAGG	1080
QY	1102	GACTTCCAATATTTCCCAAAATTTCTATGCGCTACTGAAAGTATTGATTTCAGAAAAAGAA	1161
DB	1081	GACTTCCAATATTTCCCAAAATTTCTATGCGCTACTGAAAGTATTGATTTCAGAAAAAGAA	1140
QY	1162	GCAAAAGAGAAAGAACTGATTAATCATCATGAAACACTGATTTGAGATG	1221
DB	1141	GCAAAAGAGAAAGAACTGATTAATCATCATGAAACACTGATTTGAGATG	1200
QY	1222	ATGGTGAATATGGAACTATCTCAGAAAGAGTGTTCCTTCTTCTTCTTCTTCTTCTTCTTCT	1281
DB	1201	ATGGTGAATATGGAACTATCTCAGAAAGAGTGTTCCTTCTTCTTCTTCTTCTTCTTCTTCT	1260
QY	1282	GAAATGATTTCTTCTCAGACCAAAACAGCTAGAAAAAATGCTTACTGACAAATATAAGC	1341
DB	1261	GAAATGATTTCTTCTCAGACCAAAACAGCTAGAAAAAATGCTTACTGACAAATATAAGC	1320
QY	1342	AAGCTTTTCCAGCAGCACTCAGAGAGAGTCAATGAAGAAACAGACAGTACCAGGAAGAA	1401
DB	1321	AAGCTTTTCCAGCAGCACTCAGAGAGAGTCAATGAAGAAACAGACAGTACCAGGAAGAA	1380
QY	1402	GCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCACAAAAAGATGATACTCC	1461
DB	1381	GCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCACAAAAAGATGATACTCC	1440
QY	1462	RACCCAGAGGAAAGACAGATGAACCCAAAGAAACAGAGCCCTATTGGAAGCCATC	1521
DB	1441	RACCCAGAGGAAAGACAGATGAACCCAAAGAAACAGAGCCCTATTGGAAGCCATC	1500
QY	1522	AGAAAAATATTGAATGTTGAAGAAACATGACAAAAAGGAAATTAAGAGATTTATGAC	1581
DB	1501	AGAAAAATATTGAATGTTGAAGAAACATGACAAAAAGGAAATTAAGAGATTTATGAC	1560
QY	1582	CTTTCAAAGATGAGAGACTTCAATAAACAGCTGATGCTTATGTTGAGAAAAAGGCATC	1641
DB	1561	CTTTCAAAGATGAGAGACTTCAATAAACAGCTGATGCTTATGTTGAGAAAAAGGCATC	1620
QY	1642	CTTGACAGGAGAGAGCGGCGCATCAAGCGCATTTTATAGACGCTCTAAAAATGGCAA	1701

Db 1621 CTTGACAGGAAGAGCCGAGGCCATCAAGCCATTTATAGCCCTGTAAAAATGGCAA 1680
QY 1702 AAGATCCAGGAGTCTTTCAACTGTTTCAGAAAAACAATAATAGCTTAAAAACACTTCTAAT 1761
Db 1681 AAGATCCAGGAGTCTTTCAACTGTTTCAGAAAAACAATAATAGCTTAAAAACACTTCTAAT 1740
QY 1762 TCTGTGATTTAAATTTTTTGACCCCAAGGGTTATTAGAAAGTCTCTGAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTTAAATTTTTTGACCCCAAGGGTTATTAGAAAGTCTCTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTTACAAGTGTAAAAACATAGCTTTCTTCCCGTAAAAACATCTCTGAAAGTAAAGT 1881
Db 1801 ACCTTTTACAAGTGTAAAAACATAGCTTTCTTCCCGTAAAAACATCTCTGAAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAAA 1876

RESULT 15
US-10-141-704-89
; Sequence 89, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C209
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 89
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-141-704-89

Query Match 92.5%; Score 1866.4; DB 12; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCGGCTACAGAACTTCAGCACCCACAGGGGGACAGCGTCCCTCTACCTGGA 81
Db 1 GTCTCGGCTACAGAACTTCAGCACCCACAGGGGGACAGCGTCCCTCTACCTGGA 60
QY 82 GACTTGTACTCCCGCGCCCAACCTGCTTATCCCTTGACCTCGAGTGTCTAGATCC 141
Db 61 GACTTGTACTCCCGCGCCCAACCTGCTTATCCCTTGACCTCGAGTGTCTAGATCC 120
QY 142 TGCAGCGCCGAGTCCCGGCCCTCTCCCGCCCAACCCACCCACCCCTCTGCTTCTCTGT 201
Db 121 TGCAGCGCCGAGTCCCGGCCCTCTCCCGCCCAACCCACCCACCCCTCTGCTTCTCTGT 180
QY 202 TTTTACTGCTCTCTTTTCAATATACAAAAGCTACAGCTCCAGAGCCGAGCGCGGCT 261
Db 181 TTTTACTGCTCTCTTTTCAATATACAAAAGCTACAGCTCCAGAGCCGAGCGCGGCT 240

QY 262 GTGACCCCAAGCCGAGCGTGGAAAGAAATGGGGTTCTCTGGGACCGGCACCTTGTGATCTCTG 321
Db 241 GTGACCCCAAGCCGAGCGTGGAAAGAAATGGGGTTCTCTGGGACCGGCACCTTGTGATCTCTG 300
QY 322 TTATGTCTCCCGATTCAGCTTTCCCAAAACCTCGAGGAAGCAAGACAAATCTCTACAT 381
Db 301 TTATGTCTCCCGATTCAGCTTTCCCAAAACCTCGAGGAAGCAAGACAAATCTCTACAT 360
QY 382 AATAGAGATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCGTGAAGCAGAAAGAAC 441
Db 361 AATAGAGATTAAGTGCAGAAAGACCTTTGAATGAACAGATTCGTGAAGCAGAAAGAAC 420
QY 442 AAGATTAAAAAACATATCTCTCCAGAAAAACAAGCCAGGTCCAGAGCAACTATTCTTTGTT 501
Db 421 AAGATTAAAAAACATATCTCTCCAGAAAAACAAGCCAGGTCCAGAGCAACTATTCTTTGTT 480
QY 502 GATACTTGAACCTGCTAAGGCCAATAACAGAAAAAGGAAAAAATTTGAGAAAGAACACAA 561
Db 481 GATACTTGAACCTGCTAAGGCCAATAACAGAAAAAGGAAAAAATTTGAGAAAGAACACAA 540
QY 562 TCTATAAGAAAGCTCCCACTTGTATATAAGTTGAATGTGGAAGATCTTGTATCAACCAAG 621
Db 541 TCTATAAGAAAGCTCCCACTTGTATATAAGTTGAATGTGGAAGATCTTGTATCAACCAAG 600
QY 622 AATCGAAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTTGGATCATAAATTTCAA 681
Db 601 AATCGAAAACTGATCGATGATTATGACTCTACTTAAGAGTGGATTTGGATCATAAATTTCAA 660
QY 682 GATGATCCAGATGGTCTTCACTCACTAGACGGGACTCTTTAACCGCTGAAGACATGTC 741
Db 661 GATGATCCAGATGGTCTTCACTCACTAGACGGGACTCTTTAACCGCTGAAGACATGTC 720
QY 742 CATAAAACTGCTGCCAGGATTTATGAAGAAATATGACAGAGCGCTGTTTACAGAGATGTT 801
Db 721 CATAAAACTGCTGCCAGGATTTATGAAGAAATATGACAGAGCGCTGTTTACAGAGATGTT 780
QY 802 TCTAAACTACTTTAATCTCGCCCTTATCACAGAAAGCCAAAGCACATACACTGGAAGATGAA 861
Db 781 TCTAAACTACTTTAATCTCGCCCTTATCACAGAAAGCCAAAGCACATACACTGGAAGATGAA 840
QY 862 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAAAGCCAAACATATATGAGGAGGATCC 921
Db 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAAAGCCAAACATATATGAGGAGGATCC 900
QY 922 AATAAGCCACAACTGGACTGAGATCAGCTGGAAGAAATACACAGAGAAAGTGACTCCA 981
Db 901 AATAAGCCACAACTGGACTGAGATCAGCTGGAAGAAATACACAGAGAAAGTGACTCCA 960
QY 982 ATGGGAGCAATTTCAAGATGGTCTTGTCTAAGGGAGAAACGATGAACACATATCTAACACA 1041
Db 961 ATGGGAGCAATTTCAAGATGGTCTTGTCTAAGGGAGAAACGATGAACACATATCTAACACA 1020
QY 1042 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1101
Db 1021 TTAACCTTGACAAATGGCTTGGAAAGGAGAACTTAAACCTACAGTGAAGACAACTTTAGG 1080
QY 1102 GACTTCCATATTTCCCAATTTCTATGCGCTACTGAAAGTATTTGATTTCAGAAAAAGAA 1161
Db 1081 GACTTCCATATTTCCCAATTTCTATGCGCTACTGAAAGTATTTGATTTCAGAAAAAGAA 1140
QY 1162 GCAAAAGAGAAAACAACTGATTATCTATCATGAAAACACTGATTGACTTTGTGAAGATG 1221
Db 1141 GCAAAAGAGAAAACAACTGATTATCTATCATGAAAACACTGATTGACTTTGTGAAGATG 1200
QY 1222 ATGGTGAATATGGAACAAATATCTCCAGAAAGAGTGTTCCTACCTTGAACAACTTTGGAT 1281
Db 1201 ATGGTGAATATGGAACAAATATCTCCAGAAAGAGTGTTCCTACCTTGAACAACTTTGGAT 1260
QY 1282 GAAATGATGCTCTTCAGACCAAAACAACTAGAAAAAATGCTACTGACAAATATAGC 1341
Db 1261 GAAATGATGCTCTTCAGACCAAAACAACTAGAAAAAATGCTACTGACAAATATAGC 1320

Db	1861	AAACATCTGAAGTAAGTGTGATGTAACCTGAGATTTTGTATACAGGAATCTTATT	1920
Qy	1921	TCTCATAGNCTTATTTATTTATATACGAGATATGTCCTTGGAAAAAGCCTTTAAT	1980
Db	1921	TCTCATAGNCTTATTTATTTATATACGAGATATGTCCTTGGAAAAAGCCTTTAAT	1980
Qy	1981	GGGCTGACGACNTAAAACTCATTCCTCTCCACGTGC	2017
Db	1981	GGGCTGACGACNTAAAACTCATTCCTCTCCACGTGC	2017
RESULT 2			
ID	AAI93836	standard; cDNA; 2792 BP.	
XX	AAI93836;		
XX	AAI93836;		
DT	06-NOV-2001	(first entry)	
XX	Human polynucleotide SEQ ID NO 13896.		
DE			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; hematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukemia;		
KW	neurotic system disorders; arthritis; inflammation; ss.		
XX			
OS	Homo sapiens.		
PN	WO200164835-A2.		
PD			
XX	07-SEP-2001.		
XX			
XX	26-FEB-2001; 2001WO-US04927.		
PF			
XX			
PR	28-FEB-2000; 2000US-0515126.		
PR	18-MAY-2000; 2000US-0577409.		
XX			
PA	(HXSE-) HXSEQ INC.		
XX			
PI	Tang YT, Liu C, Drmanac RT;		
XX			
DR	WPI: 2001-514838/56.		
XX	P-PSDB; AAO13903.		
PT			
PT	Isolated nucleic acids and polypeptides, useful for preventing		
PT	diagnosing and treating e.g. leukemia, inflammation and immune		
PT	disorders -		
XX			
PS	Claim 1: SEQ ID NO 13896; 1399p + Sequence Listing; English.		
XX			
XX	The invention relates to human polynucleotides (AAI79941-AAI93841) and		
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, hematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activation/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
SO	Sequence 2792 BP; 966 A; 577 C; 552 G; 697 T; 0 other;		
Query Match	95.0%; Score 1916.6; DB 22; Length 2792;		
Best Local Similarity	98.8%; Pred. No. 0;		
Matches 1993; Conservative	0; Mismatches 17; Indels 8; Gaps 6;		
QY	1 TAAAGCTACGCGCTGGC-CGCAGTCCTCCGCTCACAGGAAGCTTACAGCCACAGGCGG	59	

Db	14	TAAGCTACGCCCTGCGCCGACAGTCTCCGGCTCACAGAACTTCAGACACCACAGGGCGG	73
QY	60	ACAGGCTCCCCCTACCTGAGACTGACATCCGCGGCGCCCAACCCCTGATTCCTT	119
Db	74	ACAGGCTCCCTCTACTGAGACTTGATGATCCGCGGCGCCCAACCCCTGATTCCTT	133
QY	120	GACCGTGAATGTACAGAGATCCCTGACGCGGCCAGTCCCGGCCCTTCGCCGCCACAC	179
Db	134	GACCGTGAATGTACAGAGATCCCTGACGCGGCCAGTCCCGGCCCTTCGCCGCCACAC	193
QY	180	CCACCCCTGAGCTTCTCTGTTTTTACTCCCTTTCATTCATTAACAAAAGTACAGC	239
Db	194	CCACCCCTGAGCTTCTCTGTTTTTACTCCCTTTCATTCATTAACAAAAGTACAGC	253
QY	240	TCAGAGACCCGACGCGCGGGCTGTGACCCCAAGCCGAGCGTGAAGAAATGGGGTTCCTCG	299
Db	254	TCAGAGACCCGACGCGCGGGCTGTGACCCCAAGCCGAGCGTGAAGAAATGGGGTTCCTCG	313
QY	300	GACCGGCACTTGGATTCTGTGTGTTAGTCTCCGATTCAGCTTTCGCCAAACCTGAGAG	359
Db	314	GACCGGCACTTGGATTCTGTGTGTTAGTCTCCGATTCAGCTTTCGCCAAACCTGAGAG	373
QY	360	AAGCCAAACAAATCTCTACATTAATAGAAATTAAGTGCAGAGAAACCTTGAATGACAA	419
Db	374	AAGCCAAACAAATCTCTACATTAATAGAAATTAAGTGCAGAGAAACCTTGAATGACAA	433
QY	420	GATTGCTTAACAGAGAAGACAAAGATTAAAAAACAATATCCCTCAGAGAAAAACAGCCAG	479
Db	434	GATTGCTTAACAGAGAAGACAAAGATTAAAAAACAATATCCCTCAGAGAAAAACAGCCAG	493
QY	480	TCAGAGCAATATCTTTTGTGTGATTAACCTGTAAGGCGAATTAACAGAAAAGAA	539
Db	494	TCAGAGCAATATCTTTTGTGTGATTAACCTGTAAGGCGAATTAACAGAAAAGAA	553
QY	540	AAAAATTAAGAAAAGAAAGACAACTGATTAAGAAAGTCCCGCACTGTGATTAAGTTGAAT	599
Db	554	AAAAATTAAGAAAAGAAAGACAACTGATTAAGAAAGTCCCGCACTGTGATTAAGTTGAAT	613
QY	600	GGAAGATTTGATTCACCAAGAAATCGAAAACTGATCATGATTTGACTCTACTTAAGAG	659
Db	614	GGAAGATTTGATTCACCAAGAAATCGAAAACTGATCATGATTTGACTCTACTTAAGAG	673
QY	660	TGGATTGGATCATAAATTTCAAGATGATTCAGAGTGTTCATCACTAGACGGGACTCC	719
Db	674	TGGATTGGATCATAAATTTCAAGATGATTCAGAGTGTTCATCACTAGACGGGACTCC	733
QY	720	TTTAAACCCCTGAAGACATTTGCCATTAATGGCTGCCAGAAATTTATGAAAGAAATGACAG	779
Db	734	TTTAAACCCCTGAAGACATTTGCCATTAATGGCTGCCAGAAATTTATGAAAGAAATGACAG	793
QY	780	AGCGGTGTTGACAAGATTGTTGTTCTTAACACTACTTAATTCGCGCCCTTATCAGAGAAAGCA	839
Db	794	AGCGGTGTTGACAAGATTGTTGTTCTTAACACTACTTAATTCGCGCCCTTATCAGAGAAAGCA	853
QY	840	AGCACAATCACTGGAAGATGGAAGTGAAGAGAGGTTTTACAAAAATTTAATCTCAAGAGAGC	899
Db	854	AGCACAATCACTGGAAGATGGAAGTGAAGAGAGGTTTTACAAAAATTTAATCTCAAGAGAGC	913
QY	900	CAACAATTTATGAGAGAGATTCCTCAATTAACCCCAAGCTGAGCTGGAATTCAGCGCTGAGAA	959
Db	914	CAACAATTTATGAGAGAGATTCCTCAATTAACCCCAAGCTGAGCTGGAATTCAGCGCTGAGAA	973
QY	960	AATACACAGAAAAGTACCTCAATGAGCAATTTCAATGATGCTGTGTAAGGAGAGAAA	1019
Db	974	AATACACAGAAAAGTACCTCAATGAGCAATTTCAATGATGCTGTGTAAGGAGAGAAA	1033
QY	1020	CGATGAAACAGTATCTAAACATTTAACTTGACAAATGGCTTGAGAAAGAGAACTAAAC	1079
Db	1034	CGATGAAACAGTATCTAAACATTTAACTTGACAAATGGCTTGAGAAAGAGAACTAAAC	1093
QY	1080	CTACAGTAAAGCAACTTTAGGAGCTTCCATATTTTCCCAATTTCTATGGCGTACTGAA	1139
Db	1094	CTACAGTAAAGCAACTTTAGGAGCTTCCATATTTTCCCAATTTCTATGGCGTACTGAA	1153

	Accession	Gene	Protein	Length
QY	1140	AACTATGTGATCTGAAAAAGAGCAAAAGAGAAAGAACACTGATTTACTATCATGAAAA	1199	
Db	1154	AAATATTGATCTGAAAAAGAGCAAAAGAGAAAGAACACTGATTTACTATCATGAAAA	1213	
QY	1200	ACTGATTGACCTTGTGAAATGATGCGTGAATATGAGAACAAATATCTCCAGAAAGAGTGCT	1255	
Db	1214	ACTGATTGACCTTGTGAAATGATGCGTGAATATGAGAACAAATATCTCCAGAAAGAGTGCT	1273	
QY	1260	TTCTTACCTTGA AAACTTGATGAAATGTTGCTCTTCAGACCAAAAACAGCTAGAAAA	1319	
Db	1274	TTCTTACCTTGA AAACTTGATGAAATGTTGCTCTCTTCAGACCAAAAACAGCTAGAAAA	1333	
QY	1320	AAATGCTACTGCAATATATAGCAACCTTTTCCACACCATTCAGAGAAAGTCAATGAGA	1379	
Db	1334	AAATGCTACTGCAATATATAGCAACCTTTTCCACACCATTCAGAGAAAGTCAATGAGA	1393	
QY	1380	AACAGACACTTACCAAGGAAGAGCAGCTAAGATGGAAAAAGAAATATGGAACCTTGAAGGA	1439	
Db	1394	AACAGACACTTACCAAGGAAGAGCAGCTAAGATGGAAAAAGAAATATGGAACCTTGAAGGA	1453	
QY	1440	TTCCACAAAAAGTATTAACCTCCAACCCAGAGAGAAAAAGACAGATGAAACCCAAAGAAAAAC	1499	
Db	1454	TTCCACAAAAAGTATTAACCTCCAACCCAGAGAGAAAAAGACAGATGAAACCCAAAGAAAAAC	1513	
QY	1500	AGAAAGCATTTTGGAAAGCCATCAGAAAAAATATTCGATATGCTTGAAGAAACATGCAAAAA	1559	
Db	1514	AGAAAGCATTTTGGAAAGCCATCAGAAAAAATATTCGATATGCTTGAAGAAACATGCAAAAA	1573	
QY	1560	GGGAAATATAAGAAAGATTTATGACCTTTCAAAGATGAGAGACTTCATCAATAACAAAGCTGA	1619	
Db	1574	GGGAAATATAAGAAAGATTTATGACCTTTCAAAGATGAGAGACTTCATCAATAACAAAGCTGA	1633	
QY	1620	TGCTTATGTGGAGAAAGCATCTTGTGACAAAGAAAGAACCGAGCCATCAAGCCATTTTA	1679	
Db	1634	TGCTTATGTGGAGAAAGCATCTTGTGACAAAGAAAGAACCGAGCCATCAAGCCATTTTA	1693	
QY	1680	TAGCAGCCTGTAAAAATGGCAAAAAGATCAGAGAGCTTTCACATGTTTCAAGAAAAACATAA	1739	
Db	1694	TAGCAGCCTGTAAAAATGGCAAAAAGATCAGAGAGCTTTCACATGTTTCAAGAAAAACATAA	1753	
QY	1740	TATAGCTTAAAAACACTTCTAAATTCGTGATTTAAAAATTTTGGACCCAAAGGTTATTGAA	1799	
Db	1754	TATAGCTTAAAAACACTTCTAAATTCGTGATTTAAAAATTTTGGACCCAAAGGTTATTGAA	1813	
QY	1800	AGTGTGAATTTACAGTAGTAAACCTTTTACAAAGTGGTTAAACATATGCTTTTCCCGT	1859	
Db	1814	AGTGTGAATTTACAGTAGTAAACCTTTTACAAAGTGGTTAAACATATGCTTTTCCCGT	1873	
QY	1860	AAAAACTATCGAAGTAAGTCTTATGTAAAGCTGAATTTTGTATACAGAAATCCCTAT	1919	
Db	1874	AAAAACTATCGAAGTAAGTCTTATGTAAAGCTGAATTTTGTATACAGAAATCCCTAT	1932	
QY	1920	TTCTCATAGCTTATATATTTATATATCAGAAATATGTTGCTTGGAAAAAGCCCTTAA	1979	
Db	1933	TTCTCATAGCTTATATATTTATATATCAGAAATATGTTGCTTGGAAAAAGCCCTTAA	1988	
QY	1980	TGGGCTGACGCTAAAACTCAATCCNCTTCCACTGTC	2017	
Db	1989	TGGGCTGACGCTTAAAA-CTCATCCCTTCTCCACTGTC	2024	
RESULT 3				
ID	AAA96353	standard; cDNA; 1893 bp.		
XX	AAA96353;			
XX	08-FEB-2001	(first entry)		
XX	cdna	encoding a novel polypeptide designated PRO5990.		
XX	Secreted protein; transmembrane protein; PRO1484; PRO4334; PRO1122;			

KW	PRO1869; PRO1887; PRO1785; PRO4355; PRO4357; PRO4405; PRO4556;
KW	PRO4352; PRO4380; PRO4354; PRO4408; PRO5737; PRO4425; PRO5900; PRO6030;
KW	PRO4424; PRO4422; PRO4430; PRO4499; tumor; obesity; diabetes;
KW	Insulinemia; kidney disorder; Bergers disease; nephropathy;
KW	Schönlein-Henoch purpura; celiac disease; dermatitis herpetiformis;
KW	Crohn's disease; ss.
XX	
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	CDS 265..1671
FT	/tag= a
PN	WO200056889-A2.
PN	
XX	
PD	28-SEP-2000.
XX	
PF	01-MAR-2000; 2000WO-USO5601.
XX	
PR	23-MAR-1999; 99US-0125774.
PR	23-MAR-1999; 99US-0125778.
PR	24-MAR-1999; 99US-0125826.
PR	31-MAR-1999; 99US-0127032.
PR	05-APR-1999; 99US-0127035.
PR	21-APR-1999; 99US-0127706.
PR	27-APR-1999; 99US-0130359.
PR	27-APR-1999; 99US-0131272.
PR	27-APR-1999; 99US-0131291.
PR	04-MAY-1999; 99US-0132371.
PR	04-MAY-1999; 99US-0132379.
PR	04-MAY-1999; 99US-0132383.
PR	25-MAY-1999; 99US-0135750.
PR	08-JUN-1999; 99US-0138166.
PR	20-JUL-1999; 99US-0144791.
PR	03-AUG-1999; 99US-0146970.
PR	09-DEC-1999; 99US-0170262.
XX	
PA	(GETH) GENENTECH INC.
PI	
PI	Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J;
PI	Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX	
DR	WPI: 2000-628263/60.
DR	P-PSDB: AAB18926.
XX	
PT	Novel secreted and transmembrane polypeptides useful for diagnosing
PT	tumour in a mammal, for identifying agonists and antagonists of the
PT	polypeptide and for therapeutic use
PS	
PS	Claim 2; Fig 35; 222pp: English.
CC	
CC	The present sequence encodes a secreted or transmembrane polypeptide.
CC	The specification describes polypeptides designated PRO1484, PRO4334,
CC	PRO1122, PRO1889, PRO1890, PRO1887, PRO1785, PRO4353, PRO4357, PRO4405,
CC	PRO4356, PRO4352, PRO4380, PRO4354, PRO4408, PRO5737, PRO4425, PRO5900,
CC	PRO6030, PRO4424, PRO4422, PRO4430 and PRO4499. PRO1889 polypeptide is
CC	useful for diagnosing tumour in a mammal. The polypeptides, their
CC	agonists and antagonists are useful treating a condition associated with
CC	expression or activity of the polypeptide. Conditions treated include
CC	obesity, diabetes or hyper-or hypo-insulinemia. The polypeptides are
CC	capable of inducing proliferation of mammalian kidney mesangial cells
CC	and are therefore useful for treating kidney disorders associated with
CC	decreased mesangial cell function such as Bergers disease or other
CC	nephropathies associated with Schönlein-Henoch purpura, celiac disease,
CC	dermatitis herpetiformis or Crohn's disease. The nucleic acids may be used
CC	to generate transgenic animals for use in development and screening of
CC	therapeutically useful reagents and also for chromosome identification
CC	and tissue typing.
XX	
SO	Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other:
Query Match	92.5%; Score 1866.4; DB 21; Length 1893;
Best Local Similarity	99.7%; Pred NO. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY      22  GTCGCCGCTCAGAGAACTTCAGACCCACAGGGCGGACGCCCTCCCTCTACTGGA  81
Db      1  GTCGCCGCTCAGAGAACTTCAGACCCACAGGGCGGACGCCCTCCCTCTACTGGA  60
QY      82  GACTTGACTCCCGCGCGCCCAACCTCTATCCCTTGACCGTGTGATGTGATGATCC  141
Db      61  GACTTGACTCCCGCGCGCCCAACCTCTATCCCTTGACCGTGTGATGTGATGATCC  120
QY     142  TGCAGCGCGCCAGTCCCGCGCTCTCCGCCCCACACCCCTCTGCTCTCTCTGT  201
Db     121  TGCAGCGCGCCAGTCCCGCGCTCTCCGCCCCACACCCCTCTGCTCTCTCTGT  180
QY     202  TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  261
Db     181  TTTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT  240
QY     262  GTGACCCCAAGCCGAGCGTGAAGAAATGGGTTCCCTCGGACCGGCACTTGTCTGTG  321
Db     241  GTGACCCCAAGCCGAGCGTGAAGAAATGGGTTCCCTCGGACCGGCACTTGTCTGTG  300
QY     322  TTATGCTCCCGATTCAGCTTTTCCCAACCTGAGAGAACCAATCTCTACAT  381
Db     301  TTATGCTCCCGATTCAGCTTTTCCCAACCTGAGAGAACCAATCTCTACAT  360
QY     382  AATGAGAAATTAAGGACAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAACAC  441
Db     361  AATGAGAAATTAAGGACAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAACAC  420
QY     442  AAGATTAATAAAACATATCTCTCAGAAAAACAGCAGTCAAGCACTATCTTTGT  501
Db     421  AAGATTAATAAAACATATCTCTCAGAAAAACAGCAGTCAAGCACTATCTTTGT  480
QY     502  GATTAATCTGAACCTGCTAAAGCAATTAACAGAAAAAATTGAGAAAGAAAGACAA  561
Db     481  GATTAATCTGAACCTGCTAAAGCAATTAACAGAAAAAATTGAGAAAGAAAGACAA  540
QY     562  TCTATTAAGAGTCCCGCACTTGATTAATGAATGAATGGAAGATGTGATCAACCAAG  621
Db     541  TCTATTAAGAGTCCCGCACTTGATTAATGAATGAATGGAAGATGTGATCAACCAAG  600
QY     622  AATCGAAAACTGATGATGATTAAGTACTCTACTAAGATGATGATGATCAATTAATTC  681
Db     601  AATCGAAAACTGATGATGATTAAGTACTCTACTAAGATGATGATGATCAATTAATTC  660
QY     682  GATGATCCAGATGCTTCTCATCTACTAGACGGGACTCTTTAACCGCTGAGACATTTGC  741
Db     661  GATGATCCAGATGCTTCTCATCTACTAGACGGGACTCTTTAACCGCTGAGACATTTGC  720
QY     742  CATAAATCGCTGCCAGATTTATGAAGAAATGACAGCCGCTTTGACAAAGTTGT  801
Db     721  CATAAATCGCTGCCAGATTTATGAAGAAATGACAGCCGCTTTGACAAAGTTGT  780
QY     802  TCTAAACTACTTAATCTCGCCTTATCAGAGAAACCAAGCATACATGGAATGGA  861
Db     781  TCTAAACTACTTAATCTCGCCTTATCAGAGAAACCAAGCATACATGGAATGGA  840
QY     862  GTAGCAGAGGTTTACAAAATTAATCTCAAGAGCAACCAATTAAGAGAGATCCC  921
Db     841  GTAGCAGAGGTTTACAAAATTAATCTCAAGAGCAACCAATTAAGAGAGATCCC  900
QY     922  AATAAGCCCAACAGCTGAGCTGAGATCAGAGTGTGAAAAATTCGAGAGAAATGACTCA  981
Db     901  AATAAGCCCAACAGCTGAGCTGAGATCAGAGTGTGAAAAATTCGAGAGAAATGACTCA  960
QY     982  ATGAGCAGAAATTCAGATGCTCTTCTAAGGAGAAAAAGATGAACATCTCTAACACA  1041
Db     961  ATGAGCAGAAATTCAGATGCTCTTCTAAGGAGAAAAAGATGAACATCTCTAACACA  1020
QY    1042  TTAACCTTGACAAATGCTTGGAAGAGAACTAAACCTTACAGTGAAGACAACTTTAG  1101
Db    1021  TTAACCTTGACAAATGCTTGGAAGAGAACTAAACCTTACAGTGAAGACAACTTTAG  1080

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QY    1102  GACTTCCAATATTTCCCAATTTCTATGCGGCTAGTGAAGAAAGTATGATTCAGAAAAAGA  1161
Db    1081  GAACTCCAAATATTTCCCAATTTCTATGCGGCTAGTGAAGAAAGTATGATTCAGAAAAAGA  1140
QY    1162  GCAAAAGAGAAAGAAACACTGATATCTATCATGAAGAACATGATGACTTTGTGAAGATG  1221
Db    1141  GCAAAAGAGAAAGAAACACTGATATCTATCATGAAGAACATGATGACTTTGTGAAGATG  1200
QY    1222  ATGTGAATATGGAACAAATATCTCAGAGAGAGGTGTTTCTTACCTTGAACCTTGGAT  1281
Db    1201  ATGTGAATATGGAACAAATATCTCAGAGAGAGGTGTTTCTTACCTTGAACCTTGGAT  1260
QY    1282  GAAATGATTTGCTCTCAGACCAAAAACAAGCTAGAAAAAATGCTACGACAAATTAAGC  1341
Db    1261  GAAATGATTTGCTCTCAGACCAAAAACAAGCTAGAAAAAATGCTACGACAAATTAAGC  1320
QY    1342  AAGCTTTTCCAGCACATCAGAGAGAGATCATGAAGAACAGACAGTACCAAGAGAGA  1401
Db    1321  AAGCTTTTCCAGCACATCAGAGAGAGATCATGAAGAACAGACAGTACCAAGAGAGA  1380
QY    1402  GCAGCTAAGATGGAAGAGATATGGAAGCTTGAAGATTCACAAAAGATGATTAATCC  1461
Db    1381  GCAGCTAAGATGGAAGAGATATGGAAGCTTGAAGATTCACAAAAGATGATTAATCC  1440
QY    1462  AACCAGGAGGAGAAACAGATGACCCAAAGGAAAAACAAGACCTATTGTGAGCCATC  1521
Db    1441  AACCAGGAGGAGAAACAGATGACCCAAAGGAAAAACAAGACCTATTGTGAGCCATC  1500
QY    1522  AGAAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGGAATTAAGATTTATGAC  1581
Db    1501  AGAAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGGAATTAAGATTTATGAC  1560
QY    1582  CTTTCAAAAGATGAGACTTCTCATTAATAACAGCTGATCTTATGTGAGAGAGGCATC  1641
Db    1561  CTTTCAAAAGATGAGACTTCTCATTAATAACAGCTGATCTTATGTGAGAGAGGCATC  1620
QY    1642  CTTGCAAGGAAGAGAGCCGAGGCGCATCAAGCCATTTATGAGCCTGTAAGAAATGGCAA  1701
Db    1621  CTTGCAAGGAAGAGAGCCGAGGCGCATCAAGCCATTTATGAGCCTGTAAGAAATGGCAA  1680
QY    1702  AAGATCCAGAGACTCTTCAACTGTTTCAGAAAAACATAATATAGCTTAAACACTCTAAT  1761
Db    1681  AAGATCCAGAGACTCTTCAACTGTTTCAGAAAAACATAATATAGCTTAAACACTCTAAT  1740
QY    1762  TCTGTGATTAATAATTTTGGACCCAGGTTATTTGAAGAGTCTGAATTTACAGTAGTTA  1821
Db    1741  TCTGTGATTAATAATTTTGGACCCAGGTTATTTGAAGAGTCTGAATTTACAGTAGTTA  1800
QY    1822  ACCTTTTCAGAGTGTGTAACATATGCTTCTCCGTAAGAAACATATCTGAAGTAAAGT  1881
Db    1801  ACCTTTTCAGAGTGTGTAACATATGCTTCTCCGTAAGAAACATATCTGAAGTAAAGT  1860
QY    1882  TGTATGTAAGCTGAGA  1897
Db    1861  TGTATGTAAGCTGAGAA  1876

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RESULT 4
 AAS21288
 ID AAS21288 standard; cDNA; 1893 BP.
 XX
 AC AAS21288;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human cDNA sequence encoding for PRO5990 polypeptide.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; periferical; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.
 XX

OS Homo sapiens.
 XX
 PN WO200140466-A2.
 XX
 PD 07-JUN-2001.
 XX
 XX 01-DEC-2000; 2000WO-US32678.
 PF
 XX 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28564.
 PR 02-DEC-1999; 99WO-US28565.
 PR 09-DEC-1999; 99US-0170262.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31243.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 10-NOV-2000; 2000WO-US30873.
 XX
 XX (GETH) GENENTECH INC.
 PA
 F1 Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
 P1 Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 P1 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI: 2001-408281/43.
 DR P-PSDB: AMU12216.
 XX
 PS Isolated, secretory and transmembrane PRO polypeptide used to detect
 PT other PRO-polypeptides, link bioactive molecules to cells expressing
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
 PT lung, breast, prostate, cervical
 XX
 PS Claim 3; Fig 89; 813pp; English.
 XX
 XX AAS21244-AAS21518 encode for novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.
 CC
 XX

SQ Sequence 1893 BP: 698 A; 389 C; 385 G; 421 T; 0 other:
 Query Match 92.5%; Score 1866.4; DB 22; Length 1893;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 22 GTCTCCGCGTCACAGAGACTTCAAGACCCACAGGCGGAGAGCGCTCCCTCTACCTGGA 81
 DB 1 GTCTCCGCGTCACAGAGAACTTCAAGACCCACAGGCGGAGAGCGCTCCCTCTACCTGGA 60
 QY 82 GACTTGACTCCCGCGGCGCCCAACCCGCTTATCCCTTGACCGTGCAGTGCAGAGATCC 141
 DB 61 GACTTGACTCCCGCGGCGCCCAACCCGCTTATCCCTTGACCGTGCAGTGCAGAGATCC 120
 QY 142 TGCAGCGCGCCAGTCCCGGCGCCCTTCCCGCCACACCCACCCCTCTGCTCTCTGT 201
 DB 121 TGCAGCGCGCCAGTCCCGGCGCCCTTCCCGCCACACCCACCCCTCTGCTCTCTGT 180
 QY 202 TTTTACTCCCTCTTTCATTCATTAACAAAAGCTACAGCTCCAGAGCCCGCGGCT 261
 DB 181 TTTTACTCCCTCTTTCATTCATTAACAAAAGCTACAGCTCCAGAGCCCGCGGCT 240
 QY 262 GTGACCCAGCGCGAGGTGGAAGATGGGGTCTCTGCGAGCCGCACTTGATTCTGTG 321
 DB 241 GTGACCCAGCGCGAGGTGGAAGATGGGGTCTCTGCGAGCCGCACTTGATTCTGTG 300
 QY 322 TTATGCTCCCGATTTCAAGCTTTCCCAACCTGAGAGAACCAAGCAATCTTACAT 381
 DB 301 TTATGCTCCCGATTTCAAGCTTTCCCAACCTGAGAGAACCAAGCAATCTTACAT 360
 QY 382 AATAGAGATTAAAGTCAGAAAGACCTTGAATGAACAGATTCTGAGAGAAAGAAC 441
 DB 361 AATAGAGATTAAAGTCAGAAAGACCTTGAATGAACAGATTCTGAGAGAAAGAAC 420
 QY 442 AAGATTAAAAAACAATATTCCTCCAGAAAAACAAGCCAGTCCAGACAACTATCTTGT 501
 DB 421 AAGATTAAAAAACAATATTCCTCCAGAAAAACAAGCCAGTCCAGACAACTATCTTGT 480
 QY 502 GATTAACCTTAACCTGTTAGGCAATTAACGAAAGAAAGAAATTTAGAAAGAACCA 561
 DB 481 GATTAACCTTAACCTGTTAGGCAATTAACGAAAGAAAGAAATTTAGAAAGAACCA 540
 QY 562 TCTATAAGAAAGCTCCCACTGTATATAAGTTGAATGGAAGATTTATTCACCAAG 621
 DB 541 TCTATAAGAAAGCTCCCACTGTATATAAGTTGAATGGAAGATTTATTCACCAAG 600
 QY 622 AATCGAAAATGATGATGATATGATGATGATGATGATGATGATGATGATGATGAT 681
 DB 601 AATCGAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 682 GATGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 741
 DB 661 GATGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720
 QY 742 CATTAATGCTGCGCAGAGATTTATGAGAAATGACAGAGCCGCTTTGACAAATGTT 801
 DB 721 CATTAATGCTGCGCAGAGATTTATGAGAAATGACAGAGCCGCTTTGACAAATGTT 780
 QY 802 TCTTAAGTAACTTAATCTGCGCCTTTATGACAGAAAGCAACATTAACATGATGA 861
 DB 781 TCTTAAGTAACTTAATCTGCGCCTTTATGACAGAAAGCAACATTAACATGATGA 840
 QY 862 GTAGCAGAGGTTTTCACAAAATTAATTCACAAAGAACCAATTTATGAGAGATGCC 921
 DB 841 GTAGCAGAGGTTTTCACAAAATTAATTCACAAAGAACCAATTTATGAGAGATGCC 900
 QY 922 AATAAGCCCAAGCTGAGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 981
 DB 901 AATAAGCCCAAGCTGAGTGAATGAGATGAGATGAGATGAGATGAGATGAGATGAG 960
 QY 982 ATGGCAGCAATTCAGATGCTTCTCTAAGGAGAAAGCAATGAGAAAGCAATCTAACCA 1041
 DB 961 ATGGCAGCAATTCAGATGCTTCTCTAAGGAGAAAGCAATGAGAAAGCAATCTAACCA 1020

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OY 1042 TTAACCTTGACAAATGGCTGGAAAGAGAGAACTAAACCTACAGTGAAGACACTTTAGC 1101
DB 1021 TTAACCTTGACAAATGGCTGGAAAGAGAACTAAACCTACAGTGAAGACACTTTAGC 1080
OY 1102 GACTTCCAAATATTTCCCAATTTCTATGCGCTACTGAAAGATATTGATTGACGAAAGAA 1161
DB 1081 GAATCCCAATATTTCCCAATTTCTATGCGCTACTGAAAGATATTGATTGACGAAAGAA 1140
OY 1162 GCAAAAGAGAAAGAAACACTGATTACTATCATGAACACAGTATTGACTTGTGAAGATG 1221
DB 1141 GCAAAAGAGAAAGAAACACTGATTACTATCATGAACACAGTATTGACTTGTGAAGATG 1200
OY 1222 ATGGGAATATGGAACAATATCTCCAGAGAGAGTGTTCCTACTCTGAAACCTGTGAT 1281
DB 1201 ATGGGAATATGGAACAATATCTCCAGAGAGAGTGTTCCTACTCTGAAACCTGTGAT 1260
OY 1282 GAAATGATTTGCTCTTCAGACCAAAACCAAGCTAGAAAAAATGCTACTGACATATTAAGC 1341
DB 1261 GAAATGATTTGCTCTTCAGACCAAAACCAAGCTAGAAAAAATGCTACTGACATATTAAGC 1320
OY 1342 AAGCTTTCCAGACCAATCATAGAGAGAGTCAATGAAGAACAGACAGTACCAAGAGAA 1401
DB 1321 AAGCTTTCCAGACCAATCATAGAGAGAGTCAATGAAGAACAGACAGTACCAAGAGAA 1380
OY 1402 GCAGTAGATGAGAAAGAAATATGAGAGCTTGAAGATTCACCAAAAGATGATTAATCC 1461
DB 1381 GCAGTAGATGAGAAAGAAATATGAGAGCTTGAAGATTCACCAAAAGATGATTAATCC 1440
OY 1462 AACCCAGAGAGAAAGACAGATGAAGACCAAGAAAGAAAGCTATTTGGAGCCATCC 1521
DB 1441 AACCCAGAGAGAAAGACAGATGAAGACCAAGAAAGAAAGCTATTTGGAGCCATCC 1500
OY 1522 AGAAAAAATATGAAATGTTGAAGAAACATGACAAAAAGGAAATTAAGATTATGAC 1581
DB 1501 AGAAAAAATATGAAATGTTGAAGAAACATGACAAAAAGGAAATTAAGATTATGAC 1560
OY 1582 CTTTCAAGATGAGAGACTTTCATCAATTAACAAGCTGATGCTTATGTGAGAAAGCATC 1641
DB 1561 CTTTCAAGATGAGAGACTTTCATCAATTAACAAGCTGATGCTTATGTGAGAAAGCATC 1620
OY 1642 CTTGCAAGAGAAAGCCGAGGCCATCAAGGCCATTTTATGAGAGCCCTGTAATAATGGCA 1701
DB 1621 CTTGCAAGAGAAAGCCGAGGCCATCAAGGCCATTTTATGAGAGCCCTGTAATAATGGCA 1680
OY 1702 AAGATCCAGAGTCTTTCACCTGTTTCAGAAAACTAATATAGCTTAAACACTTCTAAT 1761
DB 1681 AAGATCCAGAGTCTTTCACCTGTTTCAGAAAACTAATATAGCTTAAACACTTCTAAT 1740
OY 1762 TCTGTGATTAATAATTTTTCAGCCCAAGGCTTATGAAGAGTCTAATTTACAGTAGTTA 1821
DB 1741 TCTGTGATTAATAATTTTTCAGCCCAAGGCTTATGAAGAGTCTAATTTACAGTAGTTA 1800
OY 1822 ACCTTTTCAGAGTGTAAACATAGCTTTCTCCCGTAATAAATCATCTGAAAGTAAAGT 1881
DB 1801 ACCTTTTCAGAGTGTAAACATAGCTTTCTCCCGTAATAAATCATCTGAAAGTAAAGT 1860
OY 1882 TGTATGTAGCTGAGA 1897
DB 1861 TGTATGTAGCTGAAA 1876

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RESULT 5
AA92132
ID AAF92132 standard; cDNA; 1893 BP.

XX AAF92132;
XX 15-MAY-2001 (first entry)
XX Human PRO5990 cDNA.
XX Human; PRO protein; mapping; ss.

```

XX OS Homo sapiens.
XX PN W0200116318-A2.
XX PD 08-MAR-2001.
XX PF 24-AUG-2000; 2000MO-US23328.
XX PR 01-SEP-1999; 99MO-US20111.
XX PR 15-SEP-1999; 99MO-US21090.
XX PR 07-DEC-1999; 99US-0169495.
XX PR 09-DEC-1999; 99US-0170262.
XX PR 11-JAN-2000; 2000MO-US04341.
XX PR 18-FEB-2000; 2000MO-US04341.
XX PR 18-FEB-2000; 2000MO-US04342.
XX PR 22-FEB-2000; 2000MO-US04414.
XX PR 01-MAR-2000; 2000MO-US05601.
XX PR 03-MAR-2000; 2000MO-US187202.
XX PR 25-APR-2000; 2000US-0199397.
XX PR 22-MAY-2000; 2000MO-US14042.
XX PR 05-JUN-2000; 2000US-0209832.
XX PA (GETH ) GENENTECH INC.
XX PI Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX DR WPI; 2001-183260/18.
XX PS P-PSDB; AAB87600.
XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in
XX PT molecular biology, including use as hybridization probes, and in
XX PT chromosome and gene mapping.
XX PS Claim 2; Fig 149; 278bp; English.
XX CC The present sequence is the coding sequence for a human PRO polypeptide
XX CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
XX CC antagonists or anti-PRO antibodies are useful for preparation of a
XX CC medicament useful in the treatment of a condition which is responsive to
XX CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
XX CC protein may also be employed as molecular weight markers for protein
XX CC electrophoresis. The PRO coding sequence has applications in molecular
XX CC biology, including use as hybridisation probes, and in chromosome and
XX CC gene mapping.
XX SQ Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;

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Query Match 92.5%; Score 1866.4; DB 22; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 22 GTCTCCGGGTACAGAGAACTTCAGACCAAGGCGGAGAGCGCTCCCTTACTCTGA 81
DB 1 GTCTCCGGGTACAGAGAACTTCAGACCAAGGCGGAGAGCGCTCCCTTACTCTGA 60
OY 82 GACTTGACTCCGCGCGGCCCAACCCCTGTTATCCCTTGAGCCGTGAGTGTGAGATCC 141
DB 61 GACTTGACTCCGCGCGGCCCAACCCCTGTTATCCCTTGAGCCGTGAGTGTGAGATCC 120
OY 142 TGCAGCGGCCCAAGTCCGCGGCCCTTCCCGCCCAACCCCTGCTGCTCTTCTCT 201
DB 121 TGCAGCGGCCCAAGTCCGCGGCCCTTCCCGCCCAACCCCTGCTGCTCTTCTCT 180
OY 202 TTTTACTCTCTCTTTTCAATATACAAAGTACAGTCCAGAGAGCCAGCGCGGCT 261
DB 181 TTTTACTCTCTCTTTTCAATATACAAAGTACAGTCCAGAGAGCCAGCGCGGCT 240
OY 262 GTGACCAAGCGGAGAGTGAAGAAATGGGTTCTCGGAGACCGGCACTTGGATTCTG 321
DB 241 GTGACCAAGCGGAGAGTGAAGAAATGGGTTCTCGGAGACCGGCACTTGGATTCTG 300

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Oy	322	TTATAGTCCCGGATTCACAGCTTTTCCCAAAACCTGGAGAGCCAAAGCAAAATCTTACAT	381
Db	301	TTATAGTCCCGGATTCACAGCTTTTCCCAAAACCTGGAGAGCCAAAGCAAAATCTTACAT	360
Oy	382	AATGAGAAATTAAGTGCAGAAAGACCCCTTGAATGAACAGATTTGCTGAAGCAGAAAGAAC	441
Db	361	AATGAGAAATTAAGTGCAGAAAGACCCCTTGAATGAACAGATTTGCTGAAGCAGAAAGAAC	420
Oy	442	AAGTTTAAAAAACATATCTCCAGAAAAACAGCCAGCTCAGAGCAACATATCTTTGGTT	501
Db	421	AAGTTTAAAAAACATATCTCCAGAAAAACAGCCAGCTCAGAGCAACATATCTTTGGTT	480
Oy	502	GATTAAGCTTGAACCTGCTTAAGGGCAATTAACGAAAGAGAAAAAATTGAGAAAGAAACACA	561
Db	481	GATTAAGCTTGAACCTGCTTAAGGGCAATTAACGAAAGAGAAAAAATTGAGAAAGAAACACA	540
Oy	562	TCTATAAGAGAGCTCCCGCACTTGATTAATTAAGTTGAATGTGGAAGATGTGATTCACACAG	621
Db	541	TCTATAAGAGAGCTCCCGCACTTGATTAATTAAGTTGAATGTGGAAGATGTGATTCACACAG	600
Oy	622	AATCGAAACCTGATGATGATTAATGATCTGATTAAGAGTGGATGGATCATTAATTTCAA	681
Db	601	AATCGAAACCTGATGATGATTAATGATCTGATTAAGAGTGGATGGATCATTAATTTCAA	660
Oy	682	GATGATCCAGAGTGGCTTTCATCACTAGACGGGACTCTTAAACCGCTGAAGACATTTGC	741
Db	661	GATGATCCAGAGTGGCTTTCATCACTAGACGGGACTCTTAAACCGCTGAAGACATTTGC	720
Oy	742	CATTAATAATGGCTGCCAGAGTTTATGAGAAAAATGACAGAGCCGTGTTTACAAAGATTGT	801
Db	721	CATTAATAATGGCTGCCAGAGTTTATGAGAAAAATGACAGAGCCGTGTTTACAAAGATTGT	780
Oy	802	TCTAAACTACTTAATCTCGGCTTATACAGAAAGCCAGACATACACTGGAAGATGAA	861
Db	781	TCTAAACTACTTAATCTCGGCTTATACAGAAAGCCAGACATACACTGGAAGATGAA	840
Oy	862	GTAGCAGAGGTTTCAAAATAATTAATCTCAAGGAAAGCCACAAATTAAGAGAGATCCC	921
Db	841	GTAGCAGAGGTTTCAAAATAATTAATCTCAAGGAAAGCCACAAATTAAGAGAGATCCC	900
Oy	922	AATTAAGCCCAACAAGCTGAGACTGAGATCAGCGCTGCAAAAAATCCAGAGAAAGTGCATCCA	981
Db	901	AATTAAGCCCAACAAGCTGAGACTGAGATCAGCGCTGCAAAAAATCCAGAGAAAGTGCATCCA	960
Oy	982	ATGGCAGCAATTCAGAGTGGTCTTCTTAAGGGAGAAAAACGATGAACAAGTATCTTAACACA	1041
Db	961	ATGGCAGCAATTCAGAGTGGTCTTCTTAAGGGAGAAAAACGATGAACAAGTATCTTAACACA	1020
Oy	1042	TTTAACCTTGACAAATGGCTGGGAAGAGAACTAAACCTCAGTGAAGACAAACCTTTAGG	1101
Db	1021	TTTAACCTTGACAAATGGCTGGGAAGAGAACTAAACCTCAGTGAAGACAAACCTTTAGG	1080
Oy	1102	GACTTCCAAATTTTCCCAAATTTCTATGCGCTACTGAAGAAATATTGATTTCAGAAAAAGAA	1161
Db	1081	GACTTCCAAATTTTCCCAAATTTCTATGCGCTACTGAAGAAATATTGATTTCAGAAAAAGAA	1140
Oy	1162	GCAAAAGAGAAAGAAACAACGTTAATCTTCATGTAAGAAACACAGATTTGACTTGTGAAGTG	1221
Db	1141	GCAAAAGAGAAAGAAACAACGTTAATCTTCATGTAAGAAACACAGATTTGACTTGTGAAGTG	1200
Oy	1222	ATGTGTGAATATGGAACAATATCTTCAGAAAGAGTGTGTTCTTCACTTGAAGAACTTGGAT	1281
Db	1201	ATGTGTGAATATGGAACAATATCTTCAGAAAGAGTGTGTTCTTCACTTGAAGAACTTGGAT	1260
Oy	1282	GAATGATTTGCTCTTCAGACCAAAAACAAGTAAAGAAAAAATGCTACTGACAAATATTAAGC	1341
Db	1261	GAATGATTTGCTCTTCAGACCAAAAACAAGTAAAGAAAAAATGCTACTGACAAATATTAAGC	1320
Oy	1342	AAGCTTTTCCAGACCATCAGAGAAGAGTATGAAGAAACAGACAGTACCAACAGAGAA	1401
Db	1321	AAGCTTTTCCAGACCATCAGAGAAGAGTATGAAGAAACAGACAGTACCAACAGAGAA	1380
Oy	1402	GCACCTAAGATGAAAAAGAAATATGAGAGCTTGAAGATTCCAAAAAGATGATTAATCTCC	1461

Db	1381	GCAGCTAAGTGGAAAGGAAATATGGAACCTTGGAAGATTCACAAAAGATGATTAACCTC	1440
Qy	1462	AACCCGAGGAGGAAAGACAGATGACCCAAAGGAAAACAGAGCCTATTGGAAGCCATC	1521
Db	1441	AACCCGAGGAGGAAAGACAGATGACCCAAAGGAAAACAGAGCCTATTGGAAGCCATC	1500
Qy	1522	AGAAAAAATATTGAATGGTTGAAGAACAATGACAAAGGGAATTAAGAAAGATTATGAC	1581
Db	1501	AGAAAAAATATTGAATGGTTGAAGAACAATGACAAAGGGAATTAAGAAAGATTATGAC	1560
Qy	1582	CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC	1641
Db	1561	CTTTCAAAGATGAGAGACTTTCATCAATAAACAAGCTGATGCTTATGTGGAGAAAGGCATC	1620
Qy	1642	CTTGACAAGGAAGAGCCGAGGCCATCAAGGCGATTTTACCAGCCGTGTAATAATGGCAA	1701
Db	1621	CTTGACAAGGAAGAGAGCCGAGGCCATCAAGGCGATTTTACCAGCCGTGTAATAATGGCAA	1680
Qy	1702	AAGATCCAGAGACTCTTTCACACTGTTTCAGAAAACATAATATAGCTTAAACACTTCAAT	1761
Db	1681	AAGATCCAGAGACTCTTTCACACTGTTTCAGAAAACATAATATAGCTTAAACACTTCAAT	1740
Qy	1762	TCGTGATTAATAATTTTGTGAACCCCAAGGTTATTAGAAGGTCGATTTTACAGTAGTA	1821
Db	1741	TCGTGATTAATAATTTTGTGAACCCCAAGGTTATTAGAAGGTCGATTTTACAGTAGTA	1800
Qy	1822	ACCTTTTACAGTGTTAACACATAGCTTCTCCGTAATAAACCTATCTGAAGTAAAGT	1881
Db	1801	ACCTTTTACAGTGTGTAAACACATAGCTTCTCCGTAATAAACCTATCTGAAGTAAAGT	1860
Qy	1882	TGTATGTAAAGTCGAGA	1897
Db	1861	TGTATGTAAAGTCGAGA	1876
RESULT 6			
ABST74452			
ID	ABST74452	standard: cDNA, 1893 BP.	
XX	AC	ABST74452;	
XX	AC		
XX	DT	10-DEC-2002 (first entry)	
DE	XX		
XX	XX		
KW	Human: ss: gene; secreted protein; transmembrane protein; antirheumatic; antiarthritic; osteopathic; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis.		
KW			
OS	Homo sapiens.		
XX	XX		
XX	PN	US2002119130-A1.	
XX	PD	29-AUG-2002.	
XX	PE	06-DEC-2001; 2001US-0006867.	
XX	PR	29-OCT-1997; 97US-063435P.	
PR	29-OCT-1997;	97US-064215P.	
PR	22-APR-1998;	98US-082797P.	
PR	29-APR-1998;	98US-083495P.	
PR	15-MAY-1998;	98US-085579P.	
PR	10-JUN-1998;	98US-088811P.	
PR	10-JUN-1998;	98US-088824P.	
PR	10-JUN-1998;	98US-088825P.	
PR	11-JUN-1998;	98US-088863P.	
PR	12-JUN-1998;	98US-089105P.	
PR	16-JUN-1998;	98US-089514P.	
PR	16-SEP-1998;	98WO-US19330.	
PR	08-MAR-1999;	99WO-US05028.	
PR	14-MAY-1999;	99WO-US10733.	
PR	02-JUN-1999;	99WO-US12252.	

PR 01-SEP-1999: 99MO-US20111.
 PR 15-SEP-1999: 99MO-US21090.
 PR 15-SEP-1999: 99MO-US21194.
 PR 22-DEC-1999: 99MO-US30720.
 PR 18-FEB-2000: 2000MO-US04341.
 PR 18-FEB-2000: 2000MO-US04342.
 PR 30-MAR-2000: 2000MO-US08439.
 PR 22-MAY-2000: 2000MO-US14042.
 PR 02-JUN-2000: 2000MO-US15264.
 PR 23-AUG-2000: 2000MO-US23522.
 PR 24-AUG-2000: 2000MO-US23328.
 PR 10-NOV-2000: 2000MO-US30873.
 PR 01-DEC-2000: 2000MO-US32378.
 PR 20-DEC-2000: 2000MO-US34956.
 PR 28-FEB-2001: 2001MO-US06520.
 PR 20-JUN-2001: 2001MO-US19692.
 PR 29-JUN-2001: 2001MO-US21066.
 PR 09-JUL-2001: 2001MO-US21735.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Eston DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI: 2002-731348/79.
 DR P-PSDB: ABG95925.
 PT
 PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating
 PT sports-related joint problems, osteoarthritis or rheumatoid arthritis
 XX
 PS Claim 2; Fig 149; 399pp; English.
 XX
 CC The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing
 CC as ABG95851-ABG95934 or their associated signal peptide, or a sequence of
 CC an extracellular domain of the proteins with their associated signal
 CC peptide or lacking its associated signal peptide. Also included are
 CC the nucleic acids encoding the proteins, vectors, host cells,
 CC fusion proteins and antibodies which specifically bind to the proteins.
 CC The proteins are useful for detecting a polypeptide designated as A, B, C
 CC or D in a sample suspected of containing an A, B, C or D polypeptide,
 CC by contacting the sample with a polypeptide designated as E, F, G, H or
 CC I (or vice versa) and determining the formation of a A/E, B/F, B/G, C/H
 CC or D/I polypeptide conjugate in the sample, where the formation of the
 CC conjugate is indicative of the presence of an A, B, C or D polypeptide
 CC in the sample, where A is a PRO10272 polypeptide, B is a PRO20110
 CC polypeptide, C is a PRO10096 polypeptide, D is a PRO19760 polypeptide,
 CC E is a PRO5801 polypeptide, F is a PRO1 polypeptide, G is a PRO20040
 CC polypeptide, H is a PRO2023 polypeptide and I is a PRO1890
 CC polypeptide. The sample comprises a cell suspected of expressing the A,
 CC B, C or D polypeptide. The E, F, G, H or I polypeptide is labeled with
 CC a detectable label or is attached to a solid support. The proteins are
 CC useful for linking a bioactive molecule to a cell expressing a
 CC polypeptide designated as A, B, C or D or E, F, G, H or I. The bioactive
 CC molecule is a toxin, a radiolabel or an antibody. The bioactive molecule
 CC causes death of the cell. A, B, C, D, E, F, G, H, or I, or antibodies
 CC against them are useful for modulating a biological activity of a cell
 CC expressing a polypeptide designated as A, B, C or D or E, F, G, H, or
 CC I. The cell is killed. The proteins are useful for identifying
 CC agonists or antagonists, for the preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the proteins, as
 CC molecular weight markers for protein electrophoresis purposes, and as
 CC therapeutic agents for treating sports-related joint problems,
 CC articular cartilage defects, osteoarthritis or rheumatoid arthritis.
 CC Nucleic acids encoding the proteins are useful as hybridisation probes,
 CC in chromosome and gene mapping, in the generation of anti-sense RNA and
 CC DNA, for the preparation of the proteins, to generate transgenic or
 CC knockout animals which are useful in the development and screening of
 CC therapeutic useful reagents, for chromosome identification, and in gene
 CC therapy. The antibody is useful as a therapeutic agent, in a diagnostic
 CC assay and for affinity purification of the protein from recombinant
 CC cell culture natural sources. The present sequence encodes a novel

CC secreted or transmembrane protein of the invention.
 XX
 SO Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;
 Query Match 92.5%; Score 1866.4; DB 24; Length 1893;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 22 GTCGCCGCTCAGACAGACTTTCAGACCCACAGGCGGAGACGCGCTCCCTCACTCGA 81
 DB 1 GTCGCCGCTCAGACAGACTTTCAGACCCACAGGCGGAGACGCGCTCCCTCACTCGA 60
 QY 82 GACTTGACTCCCGGGCGCCCAACCCGCTTATCCCTTGACCCGCTGAGTGCAGATTC 141
 DB 61 GACTTGACTCCCGGGCGCCCAACCCGCTTATCCCTTGACCCGCTGAGTGCAGATTC 120
 QY 142 TGCAGCCGCGCAGTCCCGGCGCCCTCTCCGCGCCGACACCCACCCCTCTGCTTCCGT 201
 DB 121 TGCAGCCGCGCAGTCCCGGCGCCCTCTCCGCGCCGACACCCACCCCTCTGCTTCCGT 180
 QY 202 TTTTACTCTCTCTTTTCAATTAACAAGACTACAGCTCCAGAGCCGCGCGGCT 261
 DB 181 TTTTACTCTCTCTTTTCAATTAACAAGACTACAGCTCCAGAGCCGCGCGGCT 240
 QY 262 GTGACCCCAAGCCGCGCTGGAAGAATGGGCTCTCCGCGGACCGGCACTTGATTCGTG 321
 DB 241 GTGACCCCAAGCCGCGCTGGAAGAATGGGCTCTCCGCGGACCGGCACTTGATTCGTG 300
 QY 322 TTAGTGTCCCGATTCAGCTTTTCCCAACCTTGAGAGCCCAATCTCTCAT 381
 DB 301 TTAGTGTCCCGATTCAGCTTTTCCCAACCTTGAGAGCCCAATCTCTCAT 360
 QY 382 AATAGAAATTAAGTGAAGAAGACTTTGAATGACAGATTCGTGAAGAGAAGAC 441
 DB 361 AATAGAAATTAAGTGAAGAAGACTTTGAATGACAGATTCGTGAAGAGAAGAC 420
 QY 442 AAGATTAAAAAATATCTCTCCGAAAGAACAGCAGAGTCAAGCACTATCTTGT 501
 DB 421 AAGATTAAAAAATATCTCTCCGAAAGAACAGCAGAGTCAAGCACTATCTTGT 480
 QY 502 GATACCTTGAACCTGCTTAAGGCAATTAACAGAAAAAATTTGAAAAAGACAA 561
 DB 481 GATACCTTGAACCTGCTTAAGGCAATTAACAGAAAAAATTTGAAAAAGACAA 540
 QY 562 TCTTAAGAAGCTCCCGCAGTGTATTAAGTGAATGAGATTTGATTAACCAAG 621
 DB 541 TCTTAAGAAGCTCCCGCAGTGTATTAAGTGAATGAGATTTGATTAACCAAG 600
 QY 622 AATGAAAGCTGATGATGATTAAGTGAATGAGATTTGATTAACCAAG 681
 DB 601 AATGAAAGCTGATGATGATTAAGTGAATGAGATTTGATTAACCAAG 660
 QY 682 GATGATCAGATGCTTTCATCAACTAGAGGAGCTCTTAAACCGCTGAAGACATTTGC 741
 DB 661 GATGATCAGATGCTTTCATCAACTAGAGGAGCTCTTAAACCGCTGAAGACATTTGC 720
 QY 742 CATTAATTCGCTGCGAGATTTTGAAGAAATATCAGAGCCGCTTTGACAGATTTGT 801
 DB 721 CATTAATTCGCTGCGAGATTTTGAAGAAATATCAGAGCCGCTTTGACAGATTTGT 780
 QY 802 TCTTAATCTACTTATTCGCGCTTATCAGAGAAAGCCACATACATCAGAGATGAA 861
 DB 781 TCTTAATCTACTTATTCGCGCTTATCAGAGAAAGCCACATACATCAGAGATGAA 840
 QY 862 GTACAGAGGTTTAAACAAATTAATCTCAAGAGAACCAATTAATGAGAGATCCC 921
 DB 841 GTACAGAGGTTTAAACAAATTAATCTCAAGAGAACCAATTAATGAGAGATCCC 900
 QY 922 AATAGCCCAACAGCTGAGTGAATCAGAGCTTGAGAAATTACAGAGAAATGATCTCA 981
 DB 901 AATAGCCCAACAGCTGAGTGAATCAGAGCTTGAGAAATTACAGAGAAATGATCTCA 960
 QY 982 ATGGCAGCAATTAAGATGCTTGTGTAAGGAGAAAAACATGAAATGATCTCAACCA 1041

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Db      961 ATGGCAGCAATTCMAATGCTCTTCTAAGGAGGAGAAACGATGAACATCTATCTACACA 1020
QY      1042 TTAACTTGACAATAGGCTTTGGAAAGAGAACCTTACAGTCAACACACTTTAG 1101
Db      1021 TTAACTTGACAATAGGCTTTGGAAAGAGAACCTTACAGTCAACACACTTTAG 1080
QY      1102 GACTTCCAAATATTTCCCAAAATTTCTATGCGCTACTGAAAAAGTATTGATTCAGAAAAAGAA 1161
Db      1081 GAACCTCCAAATATTTCCCAAAATTTCTATGCGCTACTGAAAAAGTATTGATTCAGAAAAAGAA 1140
QY      1162 GCAAAAAGAGAAAGAAACACTGATTAATCATCAAGAAACCTATGACTTTGTGAAGATG 1221
Db      1141 GCAAAAAGAGAAAGAAACACTGATTAATCATCAAGAAACCTATGACTTTGTGAAGATG 1200
QY      1222 ATGGTGAATATGGAACATATCTCCAGAGAGGTTTCTTACTTGAACCTTGAT 1281
Db      1201 ATGGTGAATATGGAACATATCTCCAGAGAGGTTTCTTACTTGAACCTTGAT 1260
QY      1282 GAAATGATGCTCTCTCAGACCAAAACAAGCTAGAAAAAAATGCTACTGACATATTAAGC 1341
Db      1261 GAAATGATGCTCTCTCAGACCAAAACAAGCTAGAAAAAAATGCTACTGACATATTAAGC 1320
QY      1342 AAGCTTTTCCAGCAGCATCAGAGAGAGTATGAAGAAACAGACAGATACCAAGAGAA 1401
Db      1321 AAGCTTTTCCAGCAGCATCAGAGAGAGTATGAAGAAACAGACAGATACCAAGAGAA 1380
QY      1402 GCAGCTAAGATGAAAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAAGC 1461
Db      1381 GCAGCTAAGATGAAAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAAGC 1440
QY      1462 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAAAGCTATTTGGAAGCATC 1521
Db      1441 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAAAGCTATTTGGAAGCATC 1500
QY      1522 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAATTAAGAAATTAAGTATGAC 1581
Db      1501 AGAAAAATATTTGAATGTTGAAGAAACATGACAAAAAGGAATTAAGAAATTAAGTATGAC 1560
QY      1582 CTTTCAAGATGAGAGACTTCATCAATTAACCAAGCTGATGTTATGAGAGAAAGCATC 1641
Db      1561 CTTTCAAGATGAGAGACTTCATCAATTAACCAAGCTGATGTTATGAGAGAAAGCATC 1620
QY      1642 CTTGACAAGAGAAAGCCGAGGCGCATTAAGCGCATTTATGACAGCCCTGTAATAATGGCAA 1701
Db      1621 CTTGACAAGAGAGAAAGCCGAGGCGCATTAAGCGCATTTATGACAGCCCTGTAATAATGGCAA 1680
QY      1702 AAGATCCAGAGAGTCTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACACTCTTAAT 1761
Db      1681 AAGATCCAGAGAGTCTTCAACTGTTTCAGAAAAACATAATATAGCTTAAAAACACTCTTAAT 1740
QY      1762 TCTGTGATTAATTTTTCAGCCCAAGGTTATTAAGAAAGTGTGATTTACAGTAGTA 1821
Db      1741 TCTGTGATTAATTTTTCAGCCCAAGGTTATTAAGAAAGTGTGATTTACAGTAGTA 1800
QY      1822 ACCTTTACAGTGTGTTAAACATAGCTTCTCCGTAATAAACTATCTGAAGTAAGT 1881
Db      1801 ACCTTTACAGTGTGTTAAACATAGCTTCTCCGTAATAAACTATCTGAAGTAAGT 1860
QY      1882 TGTATGTAAAGCTGAGA 1897
Db      1861 TGTATGTAAAGCTGAGA 1876
```

RESULT 7
ID ACA06116 standard; cDNA; 1893 BP.

AC ACA06116;
XX
DT 02-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #18.

```
XX      XX      Human; PRO polypeptide; secreted and transmembrane protein; cancer;  
KW      KW      non-insulin dependent diabetes mellitus; septic shock; stroke;  
KW      KW      rheumatoid arthritis; graft-versus-host disease; cardiac ischaemia;  
KW      KW      psoriasis; inflammatory bowel disease; asthma; antidiabetic;  
KW      KW      cytosolic; immunosuppressive; antineumatic; antirheumatic;  
KW      KW      cerebroprotective; vasotropic; antipsoriatic; antiinflammatory;  
KW      KW      antischismatic; gene therapy; gene; ss.  
OS      Homo sapiens.  
PN      US2003008348-A1.  
PD      09-JAN-2003.  
XX      XX      26-DEC-2001; 2001US-0035855.  
PF      14-MAY-1999; 99WO-US10733.  
PR      02-DEC-1999; 99WO-US28551.  
PR      22-DEC-1999; 99WO-US30720.  
PR      01-MAR-2000; 2000WO-US05601.  
PR      02-MAR-2000; 2000WO-US05841.  
PR      22-MAY-2000; 2000WO-US14042.  
PR      02-JUN-2000; 2000WO-US15264.  
PR      23-AUG-2000; 2000WO-US23522.  
PR      24-AUG-2000; 2000WO-US23328.  
PR      01-DEC-2000; 2000WO-US32678.  
PR      01-JUN-2001; 2001WO-US17800.  
PR      20-JUN-2001; 2001WO-US19692.  
PR      29-JUN-2001; 2001WO-US21066.  
PR      09-JUL-2001; 2001WO-US21735.  
PR      15-MAY-1998; 98US-085579P.  
PR      15-DEC-1998; 98US-112514P.  
PR      22-DEC-1998; 98US-113300P.  
PR      23-DEC-1998; 98US-113430P.  
PR      23-DEC-1998; 98US-113605P.  
PR      22-JAN-1999; 99US-116843P.  
PR      23-MAR-1999; 99US-125774P.  
PR      23-MAR-1999; 99US-125778P.  
PR      24-MAR-1999; 99US-125826P.  
PR      05-APR-1999; 99US-127035P.  
PR      13-APR-1999; 99US-127066P.  
PR      21-APR-1999; 99US-129122P.  
PR      25-MAY-1999; 99US-130359P.  
PR      08-JUN-1999; 99US-135750P.  
PR      20-JUL-1999; 99US-138166P.  
PR      03-AUG-1999; 99US-144791P.  
PR      29-OCT-1999; 99US-146970P.  
PR      16-AUG-2001; 2001US-0931836.  
XX      XX      (GETH ) GEMENTECH INC.  
PI      Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,  
PI      Stewart TA, Watanabe CK, Wood WJ, Zhang Z;  
XX      WPI: 2003-341326/32.  
DR      P-PSDB; AB069097.  
XX      XX      New PRO polypeptides and nucleic acid molecules, useful for diagnosing  
PT      or treating diabetes mellitus, cancers, septic shock, inflammatory  
PT      bowel disease or asthma, or in gene therapy, chromosome identification  
PS      or tissue typing  
PS      Claim 2; Fig 35; 196pp; English.  
CC      The present invention relates to the isolation of novel human PRO  
CC      polypeptides, and the polynucleotide sequences encoding them. The  
CC      PRO polypeptides are secreted and transmembrane proteins. The PRO  
CC      polypeptides and polynucleotides are useful in diagnosing or  
CC      treating non-insulin dependent diabetes mellitus, cancers, septic  
CC      shock, rheumatoid arthritis, graft-versus-host disease, stroke, cardiac  
CC      ischaemia, psoriasis, inflammatory bowel disease or asthma. The PRO
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CC polynucleotide sequences may be used as hybridisation probes in
CC chromosome and gene mapping, or in generating antisense RNA and DNA.
CC They are also useful in preparing PRO polypeptides, in assays to
CC identify other proteins or molecules involved in binding reactions, to
CC generate transgenic animals or knockout animals, which in turn are
CC useful in the development and screening of therapeutically useful
CC reagents, for chromosome identification, and tissue typing. The PRO
CC polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. Anti-PRO antibodies may be used in diagnostic assays for
CC PRO polypeptides, or for the affinity purification of the polypeptides
CC from recombinant cell culture or natural sources. The present sequence
CC represents a cDNA encoding a human PRO polypeptide of the invention.
xx

Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other:

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

OY 22 GTCTCCGGCTACAGAGAACTTACGACCCACAGGGGAGACAGCGCTCCCTCTACTGSA 81
Db 1 GTCTCCGGCTACAGAGAACTTACGACCCACAGGGGAGACAGCGCTCCCTCTACTGSA 60
OY 82 GACTTGACTCCCGGGGCGCCCAACCGCTTATCCCTGACCGCTGAGTGTCAAGATCC 141
Db 61 GACTTGACTCCCGGGGCGCCCAACCGCTTATCCCTGACCGCTGAGTGTCAAGATCC 120
OY 142 TGCAGCCGCCAGTCCCGGCCCTCTCCGCCCCACACCCACCTCTGGCTCTTCTGT 201
Db 121 TGCAGCCGCCAGTCCCGGCCCTCTCCGCCCCACACCCACCTCTGGCTCTTCTGT 180
OY 202 TTTTACTCTCTCTTTTCAATTAACAAGCTACAGTCCAGAGCCCGAGCGCGCT 261
Db 181 TTTTACTCTCTCTTTTCAATTAACAAGCTACAGTCCAGAGCCCGAGCGCGCT 240
OY 262 GTGACCCCAAGCGAGCGTGAAGAAATGGGTTCTCCGGGACCGGACTTGATCTGGTG 321
Db 241 GTGACCCCAAGCGAGCGTGAAGAAATGGGTTCTCCGGGACCGGACTTGATCTGGTG 300
OY 322 TTAAGTCTCCGATTCAGAGCTTTCCCAACCTGGAGAGCCAGCAAAATCTCTACAT 381
Db 301 TTAAGTCTCCGATTCAGAGCTTTCCCAACCTGGAGAGCCAGCAAAATCTCTACAT 360
OY 382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGACAGATTGCTGAAACGAGAGAC 441
Db 361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGACAGATTGCTGAAACGAGAGAC 420
OY 442 AAGATTAAATAAATCATATCTCCAGAAAACAAGCGTCAAGAGCACTATTCTTGT 501
Db 421 AAGATTAAATAAATCATATCTCCAGAAAACAAGCGTCAAGAGCACTATTCTTGT 480
OY 502 GATAAATCTGAACCTGCTAAGGCAATAACAGAAAAGAAAATTGAGAAAGAAAGACA 561
Db 481 GATAAATCTGAACCTGCTAAGGCAATAACAGAAAAGAAAATTGAGAAAGAAAGACA 540
OY 562 TCTATAGAAAGCTCCCACTTGATTAATGATTGAATGGAAAGATTGATTCACCAAG 621
Db 541 TCTATAGAAAGCTCCCACTTGATTAATGATTGAATGGAAAGATTGATTCACCAAG 600
OY 622 AATGCAAAAGTATGATGATTAATGATCTACTAGAGTGGATGGATCATTAATTGCA 681
Db 601 AATGCAAAAGTATGATGATTAATGATCTACTAGAGTGGATGGATCATTAATTGCA 660
OY 682 GATGATCCAGATGATCTATCACTACAGGAGACTCTTTAAACCGCTGAAGACATGTC 741
Db 661 GATGATCCAGATGATCTATCACTACAGGAGACTCTTTAAACCGCTGAAGACATGTC 720
OY 742 CATAAATCGCTGCCAGATTTATGAGAAAATGACAGCCGTGTTGACAAAGTTGTT 801
Db 721 CATAAATCGCTGCCAGATTTATGAGAAAATGACAGCCGTGTTGACAAAGTTGTT 780
OY 802 TCTAAACTACTTAATCTCGGCTTATCAAGAAAACCAAGCACTACACTGGAATGAA 861
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Db 781 TCTAAACTACTTAATCTCGGCTTATCAAGAAAACCAAGCACTACACTGGAATGAA 840
OY 862 GTAGCAGAGGTTTACAAAATTAATCTCAAGAGAACCAACAATTATGAGAGATCCC 921
Db 841 GTAGCAGAGGTTTACAAAATTAATCTCAAGAGAACCAACAATTATGAGAGATCCC 900
OY 922 AATAAGCCCAAGCTGACATGAGATAGCTGGAATAATTCAGAGAAAGTGACTCA 981
Db 901 AATAAGCCCAAGCTGACATGAGATAGCTGGAATAATTCAGAGAAAGTGACTCA 960
OY 982 ATGGCAGCAATTCAGATGCTTCTGTAAGGAGAAAACGATGAACAGTATCTACACA 1041
Db 961 ATGGCAGCAATTCAGATGCTTCTGTAAGGAGAAAACGATGAACAGTATCTACACA 1020
OY 1042 TTAACCTTGACAAATGCTTGGAAGAGAACTAAACCTACAGTGAAGACACTTTAGG 1101
Db 1021 TTAACCTTGACAAATGCTTGGAAGAGAACTAAACCTACAGTGAAGACACTTTAGG 1080
OY 1102 GACTTCCAAATTTTCCCAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAGAA 1161
Db 1081 GAACTCCAAATTTTCCCAATTTCTATGCGCTACTGAAAAGTATTGATTCAGAAAAGAA 1140
OY 1162 GCAAAAGAGAAAAGAACTGATTTACTATCATGAAAACACTGATTGACTTTGTGAATG 1221
Db 1141 GCAAAAGAGAAAAGAACTGATTTACTATCATGAAAACACTGATTGACTTTGTGAATG 1200
OY 1222 ATGGTAATATGGAACATATCTCCAGAAAGAGTGTTCCTACCTTGAAACCTGGAT 1281
Db 1201 ATGGTAATATGGAACATATCTCCAGAAAGAGTGTTCCTACCTTGAAACCTGGAT 1260
OY 1282 GAATGATTTGCTCTTCAACCAAAAACAAAGCTAGAAAAAATGCTACTGACAAATTAAGC 1341
Db 1261 GAATGATTTGCTCTTCAACCAAAAACAAAGCTAGAAAAAATGCTACTGACAAATTAAGC 1320
OY 1342 AAGCTTTTCCAGACCATCAGAGAGAGAGTCAATGAAGAAACAGACAGTACCAGAAAGAA 1401
Db 1321 AAGCTTTTCCAGACCATCAGAGAGAGAGTCAATGAAGAAACAGACAGTACCAGAAAGAA 1380
OY 1402 GCAGCTAAGATGAAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAATCTCC 1461
Db 1381 GCAGCTAAGATGAAAAGAAATATGGAAGCTTGAAGATTCACAAAAGATGATTAATCTCC 1440
OY 1462 AACCCAGAGAGAAAGACAGATGAACCCAAAGGAAAACAGAAAGCTATTGGAAGCCATC 1521
Db 1441 AACCCAGAGAGAAAGACAGATGAACCCAAAGGAAAACAGAAAGCTATTGGAAGCCATC 1500
OY 1522 AGAAAATATTTGAATGTTGAGAAACATGACAAAAGGAAATTAAGAGATTATGAC 1581
Db 1501 AGAAAATATTTGAATGTTGAGAAACATGACAAAAGGAAATTAAGAGATTATGAC 1560
OY 1582 CTTTCAAGATGAGAGACTTATCAATTAACAGCTGATGCTTATGTGAGAAAGGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTATCAATTAACAGCTGATGCTTATGTGAGAAAGGCATC 1620
OY 1642 CTTGACAGAGAAAGCCGAGGCCATCAAGGCGATTTTACAGGCTTTAAATAATGGCA 1701
Db 1621 CTTGACAGAGAAAGCCGAGGCCATCAAGGCGATTTTACAGGCTTTAAATAATGGCA 1680
OY 1702 AAGATCCAGAGCTTTTCAAGCTGTTGAAAACATAATATAGCTTAAACACTTCTAT 1761
Db 1681 AAGATCCAGAGCTTTTCAAGCTGTTTCAAGGAAACATAATATAGCTTAAACACTTCTAT 1740
OY 1762 TCTGTATTAATAATTTTGAAGCCCAAGGTTATTAAGAAAGTGTGAATTTACAGTAGTTA 1821
Db 1741 TCTGTATTAATAATTTTGAAGCCCAAGGTTATTAAGAAAGTGTGAATTTACAGTAGTTA 1800
OY 1822 ACCTTTTCAAGTGTTAACATATGCTTTCTCCGTTAAAAACATATCTGAAGTAAGT 1881
Db 1801 ACCTTTTCAAGTGTTAACATATGCTTTCTCCGTTAAAAACATATCTGAAGTAAGT 1860
OY 1882 TGTATTAAGCTGAGA 1897
Db 1861 TGTATTAAGCTGAGA 1840
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DB 1861 TGATGTAGCTGAAA 1876

RESULT 8
ACAO6173
ID ACA06173 standard; cDNA; 1893 BP.
XX
AC ACA06173;
XX
DT 02-JUN-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #18.
XX
XX Human; secreted and transmembrane protein; bone disorder; obesity;
KW cartilage disorder; sports injury; arthritis; diabetes mellitus;
KW hypo-insulinaemia; obesity; hyper-insulinaemia; thalassemia;
KW haemoglobin-associated disorder; kidney disorder; Berger disease;
KW mesangial cell function; nephropathy; Schonlein-Henoch purpura;
KW celiac disease; dermatitis herpetiformis; Crohn's disease;
KW anorectic; antiarthritic; antidiabetic; antianemic; nephrotoxic;
KW antiinflammatory; gene therapy; gene; ss.
OS Homo sapiens.
XX
XX US2003032061-A1.
XX
PD 13-FEB-2003.
XX
PF 26-DEC-2001; 2001US-0036214.
XX
PR 14-MAY-1999; 99WO-US07733.
PR 02-DEC-1999; 99WO-US28551.
PR 22-DEC-1999; 99WO-US30720.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 23-AUG-2000; 2000WO-US33524.
PR 24-AUG-2000; 2000WO-US33328.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 15-MAY-1998; 98US-085579P.
PR 15-DEC-1998; 98US-112514P.
PR 22-DEC-1998; 98US-113300P.
PR 23-DEC-1998; 98US-113430P.
PR 23-DEC-1998; 98US-113605P.
PR 23-DEC-1998; 98US-113621P.
PR 23-DEC-1998; 98US-114140P.
PR 12-JAN-1999; 99US-115552P.
PR 22-JAN-1999; 99US-116843P.
PR 23-MAR-1999; 99US-125774P.
PR 23-MAR-1999; 99US-125778P.
PR 24-MAR-1999; 99US-125826P.
PR 31-MAR-1999; 99US-127035P.
PR 05-APR-1999; 99US-127706P.
PR 13-APR-1999; 99US-129122P.
PR 21-APR-1999; 99US-130359P.
PR 27-APR-1999; 99US-131270P.
PR 27-APR-1999; 99US-131272P.
PR 27-APR-1999; 99US-131291P.
PR 04-MAY-1999; 99US-132371P.
PR 04-MAY-1999; 99US-132379P.
PR 04-MAY-1999; 99US-132383P.
PR 25-MAY-1999; 99US-135750P.
PR 08-JUN-1999; 99US-138166P.
PR 20-JUL-1999; 99US-144791P.
PR 03-AUG-1999; 99US-146970P.
PR 29-OCT-1999; 99US-162506P.

PR 16-AUG-2001; 2001US-0931836.
XX
XX (GETH) GENENTECH INC.
XX
XX Desnoyers L, Eaton DL, Goddard A, Godowski PJ, Gurney AL, Pan J,
PI Stewart TA, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI: 2003-341962/32.
DR P-PSDB; AB069120.
XX
PT Novel isolated PRO polypeptides e.g., PRO4334, PRO1122, PRO1899,
PT PRO1890, PRO1887, PRO1785, PRO4353, useful for treating sports
PI injuries, arthritis, diabetes, obesity, hyper- or hypo-insulinaemia -
XX
XX Claim 2; Fig 35; 194pp: English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The
CC PRO polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful in diagnosing or
CC treating various bone and/or cartilage disorders (e.g. sports
CC injuries, arthritis), various insulin deficient states (e.g. diabetes
CC mellitus, hypo-insulinaemia), obesity, hyper-insulinaemia,
CC haemoglobin-associated disorders (e.g. thalassemias), kidney disorders
CC or other nephropathies associated with Schonlein-Henoch purpura,
CC celiac disease, dermatitis herpetiformis or Crohn's disease. The PRO
CC polynucleotide sequences may be used as hybridisation probes in
CC chromosome and gene mapping, or in generating antisense RNA and DNA.
CC They are also useful in preparing PRO polypeptides, in assays to
CC identify other proteins or molecules involved in binding reaction, to
CC generate transgenic animals or knockout animals, which in turn are
CC useful in the development and screening of therapeutically useful
CC reagents, for chromosome identification, and tissue typing. The PRO
CC polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. Anti-PRO antibodies may be used in diagnostic assays for
CC PRO polypeptides, or for the affinity purification of the polypeptides
CC from recombinant cell culture or natural sources. The present sequence
CC represents a cDNA encoding a human PRO polypeptide of the invention.
XX
SQ Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGCGTACAGAACTTCAGACCAAGGCGGAGAGGCTCCCTCTACCTGGA 81
DB 1 GTCTCCGCGTACAGAACTTCAGACCAAGGCGGAGAGGCTCCCTCTACCTGGA 60
QY 82 GACTTGACATCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 141
DB 61 GACTTGACATCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
QY 142 TGCAGCGCGCGAGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 201
DB 121 TGCAGCGCGCGAGTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 180
QY 202 TTTTACTCTCTCTTTTCAATTAACAAAGCTACAGCTCCAGAGCCGCGGCGGCT 261
DB 181 TTTTACTCTCTCTTTTCAATTAACAAAGCTACAGCTCCAGAGCCGCGGCGGCT 240
QY 262 GTGACCCAGCGGAGCGTGAAGAAAGGCTTCCTCGGAGCGGAGCTTGTGCGG 321
DB 241 GTGACCCAGCGGAGCGTGAAGAAAGGCTTCCTCGGAGCGGAGCTTGTGCGG 300
QY 322 TTAGTGTCTCCGATTCAGCTTTCCCAAACTGGAGAGGCAAGCAAAATCTTACAT 381
DB 301 TTAGTGTCTCCGATTCAGCTTTCCCAAACTGGAGAGGCAAGCAAAATCTTACAT 360
QY 382 AATAGAGATTAAAGTCAGAAAGACCTTGAATGACAGATTGCTGAAGCAGAGAGAC 441


```

Db 361 AATAGAGATTAAAGTCAGAAAAGACCTTGAATGACAGATTGCTGAAGCAGAAAGAC 420
QY 442 AAGATTAAAAAACATATCTCCAGAAAACAGCCAGTCCAGAGCACTATTCTTTGTT 501
Db 421 AAGATTAAAAAACATATCTCCAGAAAACAGCCAGTCCAGAGCACTATTCTTTGTT 480
QY 502 GATACTGAAACCTGCTTAAGGCAATTAACAGAAAAGAAAAAATTGAGAAAAGAACAA 561
Db 481 GATACTGAAACCTGCTTAAGGCAATTAACAGAAAAGAAAAAATTGAGAAAAGAACAA 540
QY 562 TCTATAGAACCTCCCACTTGATTAATAGTTGATGGAAGATGTTGATTCACCAAG 621
Db 541 TCTATAGAACCTCCCACTTGATTAATAGTTGATGGAAGATGTTGATTCACCAAG 600
QY 622 AATGAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 681
Db 601 AATGAAAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
QY 682 GATGATCCAGATGGCTTCATCACTAGACGGGACTCTTTAACCGCTGAAGACATGTC 741
Db 661 GATGATCCAGATGGCTTCATCACTAGACGGGACTCTTTAACCGCTGAAGACATGTC 720
QY 742 CATAAATCGCTGCCAGATTATGAGAAAATGACAGAGCCGTGTTGACAAAGATTGT 801
Db 721 CATAAATCGCTGCCAGATTATGAGAAAATGACAGAGCCGTGTTGACAAAGATTGT 780
QY 802 TCTAACTACTTAACTCTGCGCTTATCAGAGAACCCAGACATACCTGAGAGATGA 861
Db 781 TCTAACTACTTAACTCTGCGCTTATCAGAGAACCCAGACATACCTGAGAGATGA 840
QY 862 GTAGAGAGGTTTACAAAATTAATCTCAAGAGAGCCAAATTAATGAGAGATGCC 921
Db 841 GTAGAGAGGTTTACAAAATTAATCTCAAGAGAGCCAAATTAATGAGAGATGCC 900
QY 922 AATAAGCCACAGCTGAGCTGAGATCAGCTGGAATAATACAGAGAAAGTACTCCA 981
Db 901 AATAAGCCACAGCTGAGCTGAGATCAGCTGGAATAATACAGAGAAAGTACTCCA 960
QY 982 ATGGCAGCAATTCAGATGCTGCTTAAGGAGAAAACGATGAACGATCTTAACCA 1041
Db 961 ATGGCAGCAATTCAGATGCTGCTTAAGGAGAAAACGATGAACGATCTTAACCA 1020
QY 1042 TTAACCTGACAAATGGCTTGAAGAGAAAGAACTAAACCTCAGTGAAGACACTTAA 1101
Db 1021 TTAACCTGACAAATGGCTTGAAGAGAAAGAACTAAACCTCAGTGAAGACACTTAA 1080
QY 1102 GACTTCCAAATTTTCCAAATTTCTATGCGCTACTGAAGAGTATGATTCAGAAAAGAA 1161
Db 1081 GACTTCCAAATTTTCCAAATTTCTATGCGCTACTGAAGAGTATGATTCAGAAAAGAA 1140
QY 1162 GCAAAAGAGAAAACACTGATTAATCAATGAAAACACTGATGATGATGATGATG 1221
Db 1141 GCAAAAGAGAAAACACTGATTAATCAATGAAAACACTGATGATGATGATGATG 1200
QY 1222 ATGGGAAATATGGAACATATCTCCAGAGAGAGTGTCTTCTACCTGAAAACCTGAT 1281
Db 1201 ATGGGAAATATGGAACATATCTCCAGAGAGAGTGTCTTCTACCTGAAAACCTGAT 1260
QY 1282 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAATAATGCTAGTGAATTAAGC 1341
Db 1261 GAAATGATGCTCTTCAGACCAAAACAAAGCTAGAAAATAATGCTAGTGAATTAAGC 1320
QY 1342 AAGCTTTTCCAGACCAATCAGAGAGAGTATGAAGAAACAGACAGTACCAAGAGAA 1401
Db 1321 AAGCTTTTCCAGACCAATCAGAGAGAGTATGAAGAAACAGACAGTACCAAGAGAA 1380
QY 1402 GCACCTAAGATGGAAGAGATATGGAAGCTTGAAGATTCACCAAAAAGATGATTAAGC 1461
Db 1381 GCACCTAAGATGGAAGAGATATGGAAGCTTGAAGATTCACCAAAAAGATGATTAAGC 1440
QY 1462 AACCCAGAGAGAAAGACAGATGAAGCCAAAGAGAAATCAGAAAGCTTATTTGAAAGCCATC 1521
Db 1441 AACCCAGAGAGAAAGACAGATGAAGCCAAAGAGAAATCAGAAAGCTTATTTGAAAGCCATC 1500

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QY 1522 AGAAAAATATTGAATGCTTGAGAGAAACATGACAAAAAGGAAATTAAGAGATTATGAC 1581
Db 1501 AGAAAAATATTGAATGCTTGAGAGAAACATGACAAAAAGGAAATTAAGAGATTATGAC 1560
QY 1582 CTTTCAAGATGAGAGACTTCATCAATTAACAGCTGATGCTTATGAGAGAAAGCATC 1641
Db 1561 CTTTCAAGATGAGAGACTTCATCAATTAACAGCTGATGCTTATGAGAGAAAGCATC 1620
QY 1642 CTTGACAGAGAGAGAGCCAGGCGCATCAAGCGCATTTATAGCAGCCTGTAATAATGCAA 1701
Db 1621 CTTGACAGAGAGAGAGCCAGGCGCATCAAGCGCATTTATAGCAGCCTGTAATAATGCAA 1680
QY 1702 AAGATCCAGAGACTCTTAACTGTTTCAGAAAACATATATAGCTTAAACACTCTAAT 1761
Db 1681 AAGATCCAGAGACTCTTAACTGTTTCAGAAAACATATATAGCTTAAACACTCTAAT 1740
QY 1762 TCTGTGATTAATAATTTTGAACCCCAAGGCTTATGAAGAGCTGAATTTACAGTAGTTA 1821
Db 1741 TCTGTGATTAATAATTTTGAACCCCAAGGCTTATGAAGAGCTGAATTTACAGTAGTTA 1800
QY 1822 ACCTTTACAGTGTTTAAACATAGCTTCTCCGTAATAAATATCTGAAGTAAAGT 1881
Db 1801 ACCTTTACAGTGTTTAAACATAGCTTCTCCGTAATAAATATCTGAAGTAAAGT 1860
QY 1882 TGTATGTAAGCTGAGA 1897
Db 1861 TGTATGTAAGCTGAGA 1876

RESULT 9
ACAS8884
ID ACAS8884 standard; cDNA, 1893 BP.
XX
ACAS8884;
XX
AC 10-JUN-2003 (first entry)
XX
DE cDNA encoding human secreted polypeptide PRO5990.
XX
KW Human; ss; gene; gene therapy; tumour; cancer.
XX
OS Homo sapiens.
XX
PN US2003013855-A1.
XX
PD 16-JAN-2003.
XX
PF 03-MAY-2002; 2002US-0063616.
XX
PR 30-DEC-1998; 98KR-0062142.
PR 08-MAR-1999; 99WO-US05028.
PR 14-MAY-1999; 99WO-US10733.
PR 30-DEC-1999; 99WO-US31274.
PR 18-FEB-2000; 2000WO-US04341.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05841.
PR 21-MAR-2000; 2000WO-US07532.
PR 22-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 24-AUG-2000; 2000WO-US23328.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 14-MAY-1999; 99US-0311832.
PR 25-AUG-1999; 99US-0380137.
PR 25-AUG-1999; 99US-0380138.
PR 25-AUG-1999; 99US-0380139.
PR 25-AUG-1999; 99US-0380142.
PR 15-SEP-1999; 99US-0397342.
PR 18-OCT-1999; 99US-0403297.

```


QY 1402 GCACCTAAGATGAAAGAAATATGAGAGCTTGAAGATTCACAAAGATGATACTCC 1461
DB 1381 GCACCTAAGATGAAAGAAATATGAGAGCTTGAAGATTCACAAAGATGATACTCC 1440
QY 1462 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAGCCATTTTGAAGCCATC 1521
DB 1441 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAGCCATTTTGAAGCCATC 1500
QY 1522 AGAAAAATATGTAATGTTGAAGAAACATCAACAAAAAGGAATTAAGAGATTATAC 1581
DB 1501 AGAAAAATATGTAATGTTGAAGAAACATCAACAAAAAGGAATTAAGAGATTATAC 1560
QY 1582 CTTTCAAGATGAGAGAGCTTCATCAATTAACAGCTGATGCTTATGTGAGAAAAGCATC 1641
DB 1561 CTTTCAAGATGAGAGAGCTTCATCAATTAACAGCTGATGCTTATGTGAGAAAAGCATC 1620
QY 1642 CTTGACAAGAAAGAGCCGAGCCATCAAGCCATTTATAGACGCTGTAAAAATGCGCA 1701
DB 1621 CTTGACAAGAAAGAGCCGAGCCATCAAGCCATTTATAGACGCTGTAAAAATGCGCA 1680
QY 1702 AAGATCCAGAGCTCTTCACTGTTTCAGAAAAATATATAGCTTAAACACTTCTAT 1761
DB 1681 AAGATCCAGAGCTCTTCACTGTTTCAGAAAAATATATAGCTTAAACACTTCTAT 1740
QY 1762 TCTGTGATTAATTTTGTACCCAGAGGCTATTAGAAAGTGTGAATTTAGAGTTA 1821
DB 1741 TCTGTGATTAATTTTGTACCCAGAGGCTATTAGAAAGTGTGAATTTAGAGTTA 1800
QY 1822 ACCTTTAAAGATGTTTAAACATAGCTTTTCCCGTAAAAACATATCTGAAGTAAAGT 1881
DB 1801 ACCTTTAAAGATGTTTAAACATAGCTTTTCCCGTAAAAACATATCTGAAGTAAAGT 1860
QY 1882 TGTATGTAGCTGAGA 1897
DB 1861 TGTATGTAGCTGAGA 1876

RESULT 10
ID ACA60437 standard; cDNA; 1893 BP.
XX ACA60437;
XX 11-JUN-2003 (first entry)
DE Novel human secreted and transmembrane protein PRO5990 cDNA.
XX
KW Human; secreted and transmembrane polypeptide; gene; ss.
KW Chromosome mapping; gene mapping; transgenic animal; knockout animal;
KW therapeutic agent screening; chromosome identification; tissue typing;
KW gene therapy.
XX Homo sapiens.
XX US2003018183-A1.
PN 23-JAN-2003.
XX
XX 01-MAY-2002; 2002US-0063512.
XX 06-DEC-2001; 2001US-0006867.
XX
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff E, Gerlitsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
XX WPI: 2003-330984/31.
XX P-PSDB; AB072026.
DR
XX New secreted and transmembrane PRO polypeptides and nucleic acid
PT molecules encoding the polypeptides, useful in gene therapy or
PT preparing a medicament for treating a condition that is responsive to

PT the PRO polypeptide or antibody
XX
XX Disclosure: Fig 149; 409pp; English.
XX
CC The invention describes novel isolated PRO polypeptides. The PRO
CC polypeptides or anti-PRO antibodies are useful in preparing a medicament
CC for treating a condition that is responsive to the PRO polypeptide or
CC antibody. The PRO nucleotide sequences may be used as hybridisation
CC probes in chromosome and gene mapping, or in generating antisense RNA
CC and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides,
CC in assays to identify other proteins or molecules involved in binding
CC reaction, to generate transgenic animals or knockout animals, which in
CC turn are useful in the development and screening of therapeutically
CC useful reagents, for chromosome identification, and tissue typing. The
CC PRO polypeptides and nucleic acid molecules are also useful in gene
CC therapy, and as molecular weight markers for protein electrophoresis
CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
CC PRO, or for the affinity purification of PRO from recombinant cell
CC culture or natural sources. This sequence encodes a novel human
CC secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other:
Query Match 92.5%; Score 1866.4; DB 25; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 22 GTCTCCGGTCACAGGAAGCTTACAGCCACAGAGGCGAGACAGCGCTCCCTTACCTGGA 81
DB 1 GTCTCCGGTCACAGGAAGCTTACAGCCACAGAGGCGAGACAGCGCTCCCTTACCTGGA 60
QY 82 GACTTGATCCCGCGCGCGCCCAACCCCTGCTTATCCCTTGACCGCTGAGTGCAGAGATCC 141
DB 61 GACTTGATCCCGCGCGCGCCCAACCCCTGCTTATCCCTTGACCGCTGAGTGCAGAGATCC 120
QY 142 TGCAGCCGCCAGTCCCGCGCGCTCTCCCGCCACAGCCACCCCTCGGCTCTTCTGT 201
DB 121 TGCAGCCGCCAGTCCCGCGCGCTCTCCCGCCACAGCCACCCCTCGGCTCTTCTGT 180
QY 202 TTTTACTCTCTCTTTCATTCATTAACAAAGCTACAGCTCAGAGAGCCAGCGCGGCT 261
DB 181 TTTTACTCTCTCTTTCATTCATTAACAAAGCTACAGCTCAGAGAGCCAGCGCGGCT 240
QY 262 GTGACCCAGAGCGAGCTGGAAGAAATGGGTTCTCCGGGACCCGCTTGGATTCTGTG 321
DB 241 GTGACCCAGAGCGAGCTGGAAGAAATGGGTTCTCCGGGACCCGCTTGGATTCTGTG 300
QY 322 TTAGTGTCCCGATTCAAGCTTTCCCAACCTGGAGAGGCAAGACAAATCTTACAT 381
DB 301 TTAGTGTCCCGATTCAAGCTTTCCCAACCTGGAGAGGCAAGACAAATCTTACAT 360
QY 382 AATAGAGATTAAGTGCAGAAAGACCTTTGATGAATGAATGCTGAAGCAGAGAGAGAC 441
DB 361 AATAGAGATTAAGTGCAGAAAGACCTTTGATGAATGAATGCTGAAGCAGAGAGAGAC 420
QY 442 AAGATTAAAAAATATATCTCCAGAAAAACAGAGCTCAGAGCACTATTCTTTTGT 501
DB 421 AAGATTAAAAAATATATCTCCAGAAAAACAGAGCTCAGAGCACTATTCTTTTGT 480
QY 502 GATACCTGAACCTGCTAAGGCAATTAACAGAAAAAGAAAAATTGAGAAAAAGACAA 561
DB 481 GATACCTGAACCTGCTAAGGCAATTAACAGAAAAAGAAAAATTGAGAAAAAGACAA 540
QY 562 TCTATAGAGAGCTCCCACTTGAATTAAGTTGAATGTGAGAGATGTTGATCAACCAAG 621
DB 541 TCTATAGAGAGCTCCCACTTGAATTAAGTTGAATGTGAGAGATGTTGATCAACCAAG 600
QY 622 AATGAAAACATGATGATGATTAATGATCTTACTAAGATGATGATGATGATCAATTTCAA 681
DB 601 AATGAAAACATGATGATGATTAATGATCTTACTAAGATGATGATGATGATCAATTTCAA 660
QY 682 GATGATCAGATGCTTCACTCACTAAGAGGAGCTCTTAAACGCTGAAGACATGTC 741

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Db      661 GATGATCCAGATGCTTTCATCATAGACGGGACTCCTTTAACCGCTGAACATGTTC 720
QY      742 CATTAATTCGCTGCCAGATTTATGAGAAATGACAGAGCCGTGTTGACAGATTGTT 801
Db      721 CATTAATTCGCTGCCAGATTTATGAGAAATGACAGAGCCGTGTTGACAGATTGTT 780
QY      802 TCTAAACTACTAATCTGCGCTTATCAGAAACGACATACACTGGAAATGAA 861
Db      781 TCTAAACTACTAATCTGCGCTTATCAGAAACGACATACACTGGAAATGAA 840
QY      862 GTAGCAGAGGTTTTCATAAATTAATTCATAAGAACCCACAAATTTATGAGAGATCCC 921
Db      841 GTAGCAGAGGTTTTCATAAATTAATTCATAAGAACCCACAAATTTATGAGAGATCCC 900
QY      922 AATAAGCCACACAGCTGGAGTGAATCAGAGCTGGAAAAATTTCCAGAGAAAGTGACTCCA 981
Db      901 AATAAGCCACACAGCTGGAGTGAATCAGAGCTGGAAAAATTTCCAGAGAAAGTGACTCCA 960
QY      982 ATGCGAGCAATTCAGATGCTTCTGCTAAGGAGAGAAACAGATGAACAGTATCTAACACA 1041
Db      961 ATGCGAGCAATTCAGATGCTTCTGCTAAGGAGAGAAACAGATGAACAGTATCTAACACA 1020
QY      1042 TTAACCTTGACAAATGGCTTGGAAAGGAACTAAACCTTACAGTGAAGACACTTTAGG 1101
Db      1021 TTAACCTTGACAAATGGCTTGGAAAGGAACTAAACCTTACAGTGAAGACACTTTAGG 1080
QY      1102 GACTTCCAATATTTCCCAATTTCTATGCTGCTACTGAAAGATTTGATTGAAAAAGAA 1161
Db      1081 GAATCCCAATATTTCCCAATTTCTATGCTGCTACTGAAAGATTTGATTGAAAAAGAA 1140
QY      1162 GCAAAAGAGAAAGAAACACTGATTTACTATCATGAAACACTGATTTGTTGTAGATG 1221
Db      1141 GCAAAAGAGAAAGAAACACTGATTTACTATCATGAAACACTGATTTGTTGTAGATG 1200
QY      1222 ATGGTAAATATGGAACAATATCTCCAGAAAGAGTGTTCCTTACCTTGGAAACTGGAT 1281
Db      1201 ATGGTAAATATGGAACAATATCTCCAGAAAGAGTGTTCCTTACCTTGGAAACTGGAT 1260
QY      1282 GAAATGATGCTCTTCAGACCMAAAGAGCTAGAAAAAATGCTACTGACATATTAAGC 1341
Db      1261 GAAATGATGCTCTTCAGACCMAAAGAGCTAGAAAAAATGCTACTGACATATTAAGC 1320
QY      1342 AAGCTTTTCCAGACCATCAGAGAAAGATCATATAAGAAACAGACAGTACCAAGAGAA 1401
Db      1321 AAGCTTTTCCAGACCATCAGAGAAAGATCATATAAGAAACAGACAGTACCAAGAGAA 1380
QY      1402 GCACCTAAGATGAAAAAGAAATATGAAAGCTTGAAGATTCACAAAGATGATTAATCC 1461
Db      1381 GCACCTAAGATGAAAAAGAAATATGAAAGCTTGAAGATTCACAAAGATGATTAATCC 1440
QY      1462 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAGCTATTTGGAAGCCATC 1521
Db      1441 AACCCAGAGAGAAAGACAGATGAACCCAAAGAAAAACAGAGCTATTTGGAAGCCATC 1500
QY      1522 AGAAAAAATATTTGAATGCTTGAAGAAACATGACAAAAAGGAAATTAAGAAAGATTTATGAC 1581
Db      1501 AGAAAAAATATTTGAATGCTTGAAGAAACATGACAAAAAGGAAATTAAGAAAGATTTATGAC 1560
QY      1582 CTTTCAAAAGATGAGAGACTTCATCAATTAACAAGCTGATCTTATGGAAGAAAGCATC 1641
Db      1561 CTTTCAAAAGATGAGAGACTTCATCAATTAACAAGCTGATCTTATGGAAGAAAGCATC 1620
QY      1642 CTTGACAGAGAAAGAACCCGAGCCATCAAGCCGATTTATAGACGCTGTAAAAATGGCAA 1701
Db      1621 CTTGACAGAGAAAGAACCCGAGCCATCAAGCCGATTTATAGACGCTGTAAAAATGGCAA 1680
QY      1702 AAGATCCAGAGATCTTTCAACGTTTCAGAAAAACATATATAGCTTAAAAACCTTTAAT 1761
Db      1681 AAGATCCAGAGATCTTTCAACGTTTCAGAAAAACATATATAGCTTAAAAACCTTTAAT 1740
QY      1762 TCTGTGATTTAAATTTTTTGAACCAAGGGTTATTTAGAAAGTGTGTAATTTACAGTATGTA 1821
Db      1741 TCTGTGATTTAAATTTTTTGAACCAAGGGTTATTTAGAAAGTGTGTAATTTACAGTATGTA 1800

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QY      1822 ACCTTTACAAAGTGGTTAAACATAGCTTTCTCCCGTAAAAACATCTGAAGTAAGT 1881
Db      1801 ACCTTTACAAAGTGGTTAAACATAGCTTTCTCCCGTAAAAACATCTGAAGTAAGT 1860
QY      1882 TGTATGTAAAGCTGACA 1897
Db      1861 TGTATGTAAAGCTGAAA 1876

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RESULT 11

ACA63447
ID ACA63447 standard; CDNA: 1893 BP.

ACA63447:

13-JUN-2003 (first entry)

CDNA encoding human PRO polypeptide #75.

Human: PRO polypeptide; secreted and transmembrane protein;
anti-PRO antibody; diagnostic assay; gene expression; gene; ss.

Homo sapiens.

US2003023042-A1.

30-JAN-2003.

01-MAY-2002; 2002US-0063502.

06-DEC-2001; 2001US-0006867.

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI: 2003-331484/31.

P-PSDB: AB072183.

Novel monoclonal antibody that binds to secreted and transmembrane polypeptide, useful for detecting and purifying the polypeptide and also for treating conditions responsive to the antibody

Disclosure: Fig 149; 408pp; English.

The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the treatment of a condition responsive to anti-PRO antibody. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ACA63373-ACA63456 represent cDNA sequences encoding the human PRO polypeptides of the invention.

Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;

Best local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```

QY      22 GTCCTCCGCTCAGAGAACTTCAGACCCACAGGGCGAGACAGCGCTCCCTTACCTGGA 81
Db      1 GTCCTCCGCTCAGAGAACTTCAGACCCACAGGGCGAGACAGCGCTCCCTTACCTGGA 60
QY      82 GACTTGACTCCGCGCGCGCCCAACCCCTGTTATCCCTTGACCGTGAAGTGCAGAGATCC 141
Db      61 GACTTGACTCCGCGCGCGCCCAACCCCTGTTATCCCTTGACCGTGAAGTGCAGAGATCC 120

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142 TGCAGCCGCGACGTCGCCGCCCTCTCCGCCCCACACCAACCTCTGGCTCTCTGT 201
121 TGCAGCCGCGACGTCGCCGCCCTCTCCGCCCCACACCAACCTCTGGCTCTCTGT 180
202 TTTTACTCTCTCTTTTCAATTAACAACAGCTACAGCTCCAGAGCCGCGGCT 261
181 TTTTACTCTCTCTTTTCAATTAACAACAGCTACAGCTCCAGAGCCGCGGCT 240
262 GTGACCCCAAGCCGAGCTGGAAGAAATGGGTTCTCGGGACCGGCACTTGTG 321
241 GTGACCCCAAGCCGAGCTGGAAGAAATGGGTTCTCGGGACCGGCACTTGTG 300
322 TTTAGTCTCCGATTTCAAGCTTTCCCAACCTGGAGAACCAAGAAATCTCTAAT 381
301 TTTAGTCTCCGATTTCAAGCTTTCCCAACCTGGAGAACCAAGAAATCTCTAAT 360
382 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACGATTTGGAAGAGAAAG 441
361 AATAGAGAAATTAAGTGCAGAAAGACCTTTGAATGAACGATTTGGAAGAGAAAG 420
442 AAGATTAAAAAACAATATCTCCAGAAAAACAAGCGTCAAGCACTATTTCTTGT 501
421 AAGATTAAAAAACAATATCTCCAGAAAAACAAGCGTCAAGCACTATTTCTTGT 480
502 GATAACTTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAATTTGAAAGAAAGAA 561
481 GATAACTTGAACCTGCTAAGGCAATAACAGAAAAAGAAAAATTTGAAAGAAAGAA 540
562 TCTTAAGAAAGACCTCCGACTGATTAATAGTTGAATGGAAGATGTTGATTAACCAAG 621
541 TCTTAAGAAAGACCTCCGACTGATTAATAGTTGAATGGAAGATGTTGATTAACCAAG 600
622 AATGAAAACTGATGATGATTAATAGCTCTAAGAGTGAATGATGATTAATTTCAA 681
601 AATGAAAACTGATGATGATTAATAGCTCTAAGAGTGAATGATGATTAATTTCAA 660
682 GATGATCCAGATGGCTTCATCACTAGAGGGAATCTTTAACCGGTAAGACATGTC 741
661 GATGATCCAGATGGCTTCATCACTAGAGGGAATCTTTAACCGGTAAGACATGTC 720
742 CATAAAAATCGCTGCGAGATTTATGAAGAAAAATGACAGGCGTGTGACAGATTTT 801
721 CATAAAAATCGCTGCGAGATTTATGAAGAAAAATGACAGGCGTGTGACAGATTTT 780
802 TCTAACTACTTAATCTCGGCTTATCAAGAAAGCCAGCAATCACTGGAAGTAA 861
781 TCTAACTACTTAATCTCGGCTTATCAAGAAAGCCAGCAATCACTGGAAGTAA 840
862 GTACAGAGGTTTAAACAAATTAATCTCAAGAGGCAACATTAATGAGAGATCCC 921
841 GTACAGAGGTTTAAACAAATTAATCTCAAGAGGCAACATTAATGAGAGATCCC 900
922 AATAGCCCAACAGCTGAGTGAATCAGGCTGAAAAATATCAGAGAAAGTACTCCA 981
901 AATAGCCCAACAGCTGAGTGAATCAGGCTGAAAAATATCAGAGAAAGTACTCCA 960
982 ATGCGACGATTTCAAGATGCTTGTCTAAGGAGAAAAAGATGAACAGATCTTAACA 1041
961 ATGCGACGATTTCAAGATGCTTGTCTAAGGAGAAAAAGATGAACAGATCTTAACA 1020
1042 TTAACCTTGACAAATGGCTTGAAGAGAACTTAAACCTACAGTGAAGAAACCTTTAG 1101
1021 TTAACCTTGACAAATGGCTTGAAGAGAACTTAAACCTACAGTGAAGAAACCTTTAG 1080
1102 GACTTCCAAATTTTCCAAATTTCTATGCGCTACTGAAAAATATGATTTGAAAAAGAA 1161
1081 GAACTCCAAATTTTCCAAATTTCTATGCGCTACTGAAAAATATGATTTGAAAAAGAA 1140
1162 GCAAAAAGAGAAAGAAACGATTAATCAATGAAGAAACGATGATTTGGAAGATG 1221
1141 GCAAAAAGAGAAAGAAACGATTAATCAATGAAGAAACGATGATTTGGAAGATG 1200
1222 ATGTTGAAATTTGAACATATCTCCAGAAAGAGTGTCTTCTACTGAAAACTTGAT 1281

1201 ATGCGAAATATGGAACATATCTCCAGAAAGAGTGTCTTCTACTGAAAACTTGAT 1260
1282 GAATGATTTGCTCTTCAAGCCAAAAACAAGCTAGAAAAAATGCTACTGACATTAAGC 1341
1261 GAATGATTTGCTCTTCAAGCCAAAAACAAGCTAGAAAAAATGCTACTGACATTAAGC 1320
1342 AAGCTTTTCCAGACACATCAAGAGAGTCAATGAAGAAACAGACATGATTAAGC 1401
1321 AAGCTTTTCCAGACACATCAAGAGAGTCAATGAAGAAACAGACATGATTAAGC 1380
1402 GCAGCTAATGAGAAAGAAATGAGAGCTTGAAGATTCACAAAGATGATTAAGC 1461
1381 GCAGCTAATGAGAAAGAAATGAGAGCTTGAAGATTCACAAAGATGATTAAGC 1440
1462 AACCCAGAGAGAAAGACATGAAACCCAAAGAAAAACAAGACCTATTGGAAGCCATC 1521
1441 AACCCAGAGAGAAAGACATGAAACCCAAAGAAAAACAAGACCTATTGGAAGCCATC 1500
1522 AGAAAAATTTGATGATGTTGAAGAAACATGACAAAAAGGAAATTAAGATTAAGC 1581
1501 AGAAAAATTTGATGATGTTGAAGAAACATGACAAAAAGGAAATTAAGATTAAGC 1560
1582 CTTTCAAGATGAGAGACTTCAATTAACAAAGCTGATGCTTATGAGAGAAAGCCATC 1641
1561 CTTTCAAGATGAGAGACTTCAATTAACAAAGCTGATGCTTATGAGAGAAAGCCATC 1620
1642 CTTGCAAGAGAAAGAAAGCCGAGGCAATCAAGGCAATTTATGAGAGCTGTAAGAAAG 1701
1621 CTTGCAAGAGAAAGAAAGCCGAGGCAATCAAGGCAATTTATGAGAGCTGTAAGAAAG 1680
1702 AAGATCCAGAGCTCTTTAACTGTTTCAAGAAACATTAATTAAGCTTAAACATTTAT 1761
1681 AAGATCCAGAGCTCTTTAACTGTTTCAAGAAACATTAATTAAGCTTAAACATTTAT 1740
1762 TCTGATTAATAATTTTGAACCAAGGCTATTAAGAAAGCTGAATTTACAGTAA 1821
1741 TCTGATTAATAATTTTGAACCAAGGCTATTAAGAAAGCTGAATTTACAGTAA 1800
1822 ACCTTTTCAAGTGGTTAAACATTAAGCTTTCTCCGTAAGAAACATTAAGTAAAGT 1881
1801 ACCTTTTCAAGTGGTTAAACATTAAGCTTTCTCCGTAAGAAACATTAAGTAAAGT 1860
1882 TGTATGTAAGCTGAGA 1897
1861 TGTATGTAAGCTGAAA 1876

RESULT 12
ACA03647
ID ACA03647 standard; cDNA; 1893 BP.
XX
XX ACA03647;
XX AC
XX 23-MAY-2003 (first entry)
DT
DE cDNA encoding human PRO polypeptide #45.
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder;
KW cytosolic; gene; ss.
XX
XX Homo sapiens.
OS
PN US2003036180-A1.
XX
XX 20-FEB-2003.
PD
XX 09-MAY-2002; 2002US-0143114.
XX PF
XX 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.

14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 16-SEP-1998; 98WO-US19177.
 PR 17-SEP-1998; 98WO-US19330.
 PR 29-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US05106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 20-APR-1999; 98WO-US05190.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 05-OCT-1999; 98WO-US21547.
 PR 29-NOV-1999; 98WO-US23089.
 PR 30-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 01-DEC-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 02-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28564.
 PR 16-DEC-1999; 98WO-US28565.
 PR 20-DEC-1999; 98WO-US30911.
 PR 22-DEC-1999; 98WO-US30989.
 PR 30-DEC-1999; 98WO-US30770.
 PR 30-DEC-1999; 98WO-US31243.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US03736.
 PR 11-FEB-2000; 2000WO-US03655.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 01-MAR-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06319.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14541.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.

PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000WO-US074259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 01-JUN-2001; 2001US-0866034.
 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.

(GETH) GENENTECH INC.

Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gertsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;
 WPI: 2003-332040/31.
 P-PSDB; AB066614.

New secreted and transmembrane PRO nucleic acids, useful for gene
 therapy, in chromosome and gene mapping, as chromosome markers, in
 tissue typing, and in chromosome identification
 Claim 2; Fig 89; 660pp; English.

The present invention relates to the isolation of novel human PRO
 polypeptides, and the polynucleotide sequences encoding them. The
 PRO polypeptides are secreted and transmembrane proteins. The PRO
 polypeptides are useful for detecting other PRO polypeptides, for
 linking bioactive molecules to cells expressing PRO polypeptides,
 for modulating biological activities of cells expressing PRO
 polypeptides, and for identifying agonists or antagonists.
 The PRO polypeptides are useful for stimulating the release of
 tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 the proliferation or differentiation of chondrocytes, and detecting the
 presence of tumours. The polynucleotide sequences encoding PRO
 polypeptides are useful as hybridisation probes. In chromosome and
 gene mapping, in the generation of antisense RNA and DNA, in the
 preparation of PRO polypeptides, for generating transgenic animals or
 knockout animals, for the genetic analysis of individuals with genetic
 disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
 encoding the human PRO polypeptides of the invention.
 Note: The sequence data for this patent was obtained in electronic
 format directly from the USPTO web site at
 seqdata.uspto.gov/psipsidentry.html.

Sequence 1893 BP; 698 A; 389 G; 385 C; 421 T; 0 other:

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 22 GTCTCCGCGTCACAGAACTTCAGACCCACAGGCGGACGCTCCCTCTACGGA 81
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Db 61 GACTTGACTCCGGCGGCCCCAACCCCTGCTTATCCCTTGACCGTGCAGTGTCAAGATCC 120
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 Db 121 TGCAGCGCGCCAGTCCGGGCCCCCTCTCCCGCCCAACCCACCTCTGCGCTTTCTCTGT 180
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 Db 181 TTTTACTGCTCTCTTTTCTTATCATTAACAAAGCTACAGTCCAGGAGGCCACGCGGGCT 240
 QY 262 GTGACCCCAAGCCGAGCGTGAAGAATGGGGTTCTCGGAGCCGCGACTTGTGATTCGTGTG 321
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 Db 481 GATTAACCTTGAACTGCTTAAGGCAATAACAGAAAAGAAAATTGAGAAAAGACAA 540
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 Db 541 TCTTAAGAAGCTCCCGACTGATTAATGAATGATGGAAGATGTTGATTCACACCAAG 600
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RESULT 13
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 ID ACA04068 standard; cDNA; 1893 BP.
 AC ACA04068;
 DT 27-MAY-2003 (first entry)
 DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 89.
 XX Human: ss: gene; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioindicator; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032155-A1.
 XX 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.

XX 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US14552.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 16-SEP-1998; 98WO-US19177.
 PR 17-SEP-1998; 98WO-US19330.
 PR 07-OCT-1998; 98WO-US19437.
 PR 29-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
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 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25106.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
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 PR 20-APR-1999; 99WO-US08615.
 PR 14-MAY-1999; 99WO-US10733.
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 PR 30-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 99WO-US31274.
 PR 06-JAN-2000; 2000WO-US00219.
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 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23528.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
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 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 18-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
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 PR 05-JUN-2001; 2001US-0872035.
 PR 14-JUN-2001; 2001US-0874503.
 PR 19-JUN-2001; 2001US-0882636.
 PR 21-JUN-2001; 2001US-0886342.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 (GENTH) GENENTECH INC.
 Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 Gertsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 WPI: 2003-331925/31.
 P-PSDB; ABU66890.
 New secreted and transmembrane nucleic acids and polypeptides,
 designated as PRO, useful for treating inflammation, organ failure,
 atherosclerosis, cardiac injury, infertility, birth defects, premature
 aging, AIDS, or cancer -
 XX
 PS Claim 2; Fig 89; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleotide sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.

CC The present sequence encodes a PRO. protein of the invention.

XX Sequence 1893 BP; 698 A; 389 C; 385 G; 421 T; 0 other;

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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OY 22 GTCCTCGGCTACAGAAACTTCAGACACCCAGGCGGAGACACGCTCCCTCTACTGTGA 81
DB 1 GTCCTCGGCTACAGAACTTCAGACACCCAGGCGGAGACACGCTCCCTCTACTGTGA 60
OY 82 GACTTGACTCCCGCGCGGCCCAACCTGCTTATCCCTTGACCGTGAAGTGCAGAGATCC 141
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OY 142 TGCAGCGCGCCAGTCCCGCGGCCCTCTCCCGCCACACACCCTCTGCTTCTGT 201
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OY 562 TCTATTAAGAAGCTCCCACTGATTAATGAAGTGAAGTGAAGATGTTGAACCAAG 621
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DB 601 AATCGAAAACCTGATGATGATTAATGACTTACTAAGAGTGAATGATCAATAATTCAA 660
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DB 721 CATTAATGCTGCGCAGATTTATGAAGAAATGACAGACCGTGTGTAACAAGATTGT 780
OY 802 TCTAAACTACTTAATGCTGCGCTTATCAGAAAAGCAAGCAATACCTGGAAGTGA 861
DB 781 TCTAAACTACTTAATGCTGCGCTTATCAGAAAAGCAAGCAATACCTGGAAGTGA 840
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DB 1801 ACCCTTTACAAAGGTTTAAACAATACCTTCTCCGCTAAACCTATCGAAAGTAAAGT 1860
OY 1882 TGTATGTAAGCTGAGA 1897
DB 1861 TGTATGTAAGCTGAAA 1876

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RESULT 14

ABX89185.
ID ABX89185 standard; cDNA; 1893 BP.

XX ABX89185;

XX AC 13-MAY-2003 (first entry)

XX DT DNA encoding novel secreted and transmembrane protein PRO590.

XX Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
OS Homo sapiens.
XX
XX US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
PR 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 16-SEP-1998; 98WO-US19177.
PR 17-SEP-1998; 98WO-US19330.
PR 07-OCT-1998; 98WO-US19437.
PR 29-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-NOV-1998; 98WO-US22992.
PR 01-DEC-1998; 98WO-US24855.
PR 05-JAN-1999; 98WO-US25108.
PR 08-MAR-1999; 99WO-US00106.
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PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
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PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000US-0747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 18-MAY-2001; 2001US-0860216.
PR 23-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0872035.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GEPH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerlitsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-148238/14.
XX P-PSDB; AB059695.
XX
XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
XX are therapeutically useful for enhancing immune response and in cancer
XX treatments
XX
XX Claim 2; Fig 89; 659pp; English.
XX
XX The invention describes an isolated human PRO polypeptide. The PRO
XX polypeptides are useful in detecting PRO polypeptides in a sample, in
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and
XX in modulating at least one biological activity of a cell expressing a PRO
XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
XX stimulate adrenal cortical capillary endothelial growth, and PRO536,
XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
XX useful for treating conditions or disorders where angiogenesis would be

CC beneficial, e.g. wound healing and antagonist of this polypeptide are
CC useful for treating cancerous tumours. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated endothelial cell growth in
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1066, PRO1384, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other's
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC sequence encodes a novel human PRO protein.

xx Sequence 1893 BP: 698 A: 389 C: 385 G: 421 T: 0 other:

Query Match 92.5%; Score 1866.4; DB 25; Length 1893;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 181 TTTTACT 240
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QY 322 TTAGTGTCTCCGATTCAGCTTTTCCCAACCTGAGGAGGCGCAAGCAATCTCTACAT 381
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QY 382 AATAGAGATTTAAGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAGAGAC 441
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DB 481 GATACTTGAACCTGCTAAGGCAATACAGAAAAAGAAAAATTTGAGAAAAAGACAA 540
QY 562 TCTATAGAGAGCTCCCACTTGATTAATAGTTGAATGTGAAGATGTTGATTCAACAG 621
DB 541 TCTATAGAGAGCTCCCACTTGATTAATAGTTGAATGTGAAGATGTTGATTCAACAG 600
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QY 682 GATGATCCAGATGCTTCTCATCACTAGACGGAGCTCTTTAAACCGTGAAGACATTTTC 741
DB 661 GATGATCCAGATGCTTCTCATCACTAGACGGAGCTCTTTAAACCGTGAAGACATTTTC 720

QY 742 CATAAATCGCTGCCAGGATTTATGAGAAAAATGACAGAGCGGTGTTGACAAATGTT 801
DB 721 CATAAATCGCTGCCAGGATTTATGAGAAAAATGACAGAGCGGTGTTGACAAATGTT 780
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DB 781 TCTAACTACTTAATCTCGGCGCTTATCAGAGAAAGCCAGAGCATACATGAGAGATGAA 840
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DB 841 GTAGCAGAGGTTTACAAAAATTAATCTCAAGAGAGCCAAACATTTATGAGAGATCCC 900
QY 922 AATAAGCCACAGGTGACATGAGATGAGATGAGTGAAGAAAAATTCAGAGAAAGTCTCCA 981
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DB 1081 GAACTTCGATATTTTCCCAATTTCTATGCGCTACAGAGAAAGATGATTCAGAAAAAGAA 1140
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QY 1462 AACCAG 1521
DB 1441 AACCAG 1500
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DB 1621 CTTGACAG 1680
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QY 1762 TCTGTATTAATTTTGTGACCAAGGTTATTAAGAAAGTGTGATTAACAGTATGTTA 1821
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QY 1822 ACCCTTTACAGTGTGTTAAACATAGCTTCTCCGTAATAAAGTGAAGT 1881
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DB 1801 ACCCTTTACAGTGTGTTAAACATAGCTTCTCCGTAATAAAGTGAAGT 1860
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RESULT 15
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ID AAK94872 standard; cDNA: 1871 BP.
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AC AAK94872;
XX
DT 06-NOV-2001 (first entry)
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DE Human full-length cDNA, SEQ ID NO: 4060.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
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PF 07-JUL-2000; 2000EP-0114089.
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PR 08-JUL-1999; 99JP-0194486.
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PR 11-JAN-2000; 2000JP-0118774.
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PR 02-MAY-2000; 2000JP-0183765.
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PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Makemitsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI: 2001-524255/58.
XX P-PSDB: AAM93910.
XX
DR 830 Primers useful for synthesizing full length cDNA clones and their
PT use in genetic manipulation -
XX
PS Claim 8; SEQ ID NO 4060; 1380bp + sequence listing; English.
XX
CC The invention relates to primers for synthesizing full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been
CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC molecules have been determined. Primers for synthesizing the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a full length
CC human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 1871 BP; 677 A; 389 C; 385 G; 420 T; 0 other;

Query Match 92.3%; Score 1861.4; DB 22; Length 1871;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1865; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 84 CTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCTGAGTGCAGAGATCCG 143
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DB 61 CTTGACTCCCGCGCGCCCAACCCCTGCTTATCCCTTGACCTGAGTGCAGAGATCCG 120
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-554-945B-2

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2384	99.3	468	12	US-10-035-977-67
3	2384	99.3	468	12	US-10-063-735-150
4	2384	99.3	468	12	US-10-137-870-80
5	2384	99.3	468	12	US-10-140-018-90
6	2384	99.3	468	12	US-10-140-021-90
7	2384	99.3	468	12	US-10-140-274-90
8	2384	99.3	468	12	US-10-140-471-90
9	2384	99.3	468	12	US-10-140-807-80
10	2384	99.3	468	12	US-10-140-922-80
11	2384	99.3	468	12	US-10-140-924-90
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14	2384	99.3	468	12	US-10-141-702-90
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16	2384	99.3	468	12	US-10-142-421-90	Sequence 90, Appl
17	2384	99.3	468	12	US-10-142-432-90	Sequence 90, Appl
18	2384	99.3	468	12	US-10-142-767-80	Sequence 90, Appl
19	2384	99.3	468	12	US-10-143-033-90	Sequence 90, Appl
20	2384	99.3	468	12	US-10-144-994-90	Sequence 90, Appl
21	2384	99.3	468	12	US-10-145-628-90	Sequence 90, Appl
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23	2384	99.3	468	12	US-10-145-633-90	Sequence 90, Appl
24	2384	99.3	468	12	US-10-145-746-90	Sequence 90, Appl
25	2384	99.3	468	12	US-10-145-748-90	Sequence 90, Appl
26	2384	99.3	468	12	US-10-145-823-90	Sequence 90, Appl
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29	2384	99.3	468	12	US-10-145-876-90	Sequence 90, Appl
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31	2384	99.3	468	12	US-10-146-724-90	Sequence 90, Appl
32	2384	99.3	468	12	US-10-146-725-90	Sequence 90, Appl
33	2384	99.3	468	12	US-10-146-795-90	Sequence 90, Appl
34	2384	99.3	468	12	US-10-147-495-90	Sequence 90, Appl
35	2384	99.3	468	12	US-10-147-501-90	Sequence 90, Appl
36	2384	99.3	468	12	US-10-147-504-90	Sequence 90, Appl
37	2384	99.3	468	12	US-10-147-506-90	Sequence 90, Appl
38	2384	99.3	468	12	US-10-147-509-90	Sequence 90, Appl
39	2384	99.3	468	12	US-10-147-510-90	Sequence 90, Appl
40	2384	99.3	468	12	US-10-147-511-90	Sequence 90, Appl
41	2384	99.3	468	12	US-10-147-529-90	Sequence 90, Appl
42	2384	99.3	468	12	US-10-152-357-90	Sequence 90, Appl
43	2384	99.3	468	12	US-10-153-586-90	Sequence 90, Appl
44	2384	99.3	468	12	US-10-158-783-90	Sequence 90, Appl
45	2384	99.3	468	12	US-10-158-786-90	Sequence 90, Appl

ALIGNMENTS

Result 1
US-09-931-836-67
Sequence 67, Application US/09931836
Publication No. US20030027249A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gueney, Austin L.
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: ZHANG, ZEMIN
TITLE OF INVENTION: ACIDED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C1
CURRENT APPLICATION NUMBER: US/09/931, 836
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22

;; PRIOR APPLICATION NUMBER: 60/125774
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/125778
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/125886
;; PRIOR FILING DATE: 1999-03-24
;; PRIOR APPLICATION NUMBER: 60/127035
;; PRIOR FILING DATE: 1999-03-31
;; PRIOR APPLICATION NUMBER: 60/127706
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: 60/129122
;; PRIOR FILING DATE: 1999-04-13
;; PRIOR APPLICATION NUMBER: 60/130359
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131270
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131272
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131291
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/132371
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: 60/132379
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: 60/132383
;; PRIOR FILING DATE: 1999-05-04
;; PRIOR APPLICATION NUMBER: 60/135750
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/138166
;; PRIOR FILING DATE: 1999-06-08
;; PRIOR APPLICATION NUMBER: 60/144791
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/146970
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/162506
;; PRIOR FILING DATE: 1999-10-29
;; PRIOR APPLICATION NUMBER: 09/311832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 09/380142
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/644848
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 09/747259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: 09/816744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: 09/854208
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/854280
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/874503
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: 09/869599
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: 09/908,827
;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: PCT/US99/28551
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30720
;; PRIOR FILING DATE: 1999-12-22
;; PRIOR APPLICATION NUMBER: PCT/US00/05601
;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: 2000-05-22
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/23522
;; PRIOR FILING DATE: 2000-08-23
;; PRIOR APPLICATION NUMBER: PCT/US00/23328

;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-06-28
;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 80
;; SEQ ID NO 67
;; LENGTH: 468
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-931-836-67

Query Match 99.3%; Score 2384; DB 11; Length 468;
Best Local Similarity 99.1%; Pred. No. 1,2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFCTGTWLVLPVLPQAFPPKPGSODKSLHNRKLSAERPLNEQIAEAEDKIKKTYPP 60
DB 1 MGFCTGTWLVLPVLPQAFPPKPGSODKSLHNRKLSAERPLNEQIAEAEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVNDNLNRAITTEKERTKERSIRSSPLDNKLNVEDVSTKRRKLIIDY 120
DB 61 ENKPGQSNYSFVNDNLNRAITTEKERTKERSIRSSPLDNKLNVEDVSTKRRKLIIDY 120
QY 121 DSTKSGLDHKEFQDDPDGLHOLDGTPLEADIVKIAARIYEENDRAVFDKIVSKLNLGL 180
DB 121 DSTKSGLDHKEFQDDPDGLHOLDGTPLEADIVKIAARIYEENDRAVFDKIVSKLNLGL 180
QY 181 ITESQATTLDEVAEVAEYQKLSKEANNYEDPPKPTSWTENQAGKIPEKVTYMAAIQDGL 240
DB 181 ITESQATTLDEVAEVAEYQKLSKEANNYEDPPKPTSWTENQAGKIPEKVTYMAAIQDGL 240
QY 241 AKGENDETYSNTLTNLNGLEPRRTKYSSEDFRDFQYEPNPFYALNLSIDSEKKEKETLI 300
DB 241 AKGENDETYSNTLTNLNGLEPRRTKYSSEDFRDFQYEPNPFYALNLSIDSEKKEKETLI 300
QY 301 TIMKTLIDFVKMVKYGTISPREGVSYLENLDEMIALQTKNLEKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMVKYGTISPREGVSYLENLDEMIALQTKNLEKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEFAKKEKEYSIKDSTKDNNSPGKCTDEPKGTAEVYEAIRKNIEMWL 420
DB 361 KSHETDSTKEFAKKEKEYSIKDSTKDNNSPGKCTDEPKGTAEVYEAIRKNIEMWL 420
QY 421 KHDKKNKEDYDLSKMRDEINKQADAYVEKGLIDKEEAPAKRITSSL 468
DB 421 KHDKKNKEDYDLSKMRDEINKQADAYVEKGLIDKEEAPAKRITSSL 468

RESULT 2
US-10-035-977-67
; Sequence 67, Application US/10035977
; Publication No. US20030134327A1
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

APPLICANT : Zhang, Zemin
TITLE OF INVENTION: SECURED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3030R1C10
CURRENT FILING DATE: 2001-12-26
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/112514
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113300
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113430
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113605
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113621
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114140
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/115552
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/116843
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/125774
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125778
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: 60/125826
PRIOR FILING DATE: 1999-03-24
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PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/127706
PRIOR FILING DATE: 1999-04-05
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PRIOR FILING DATE: 1999-04-13
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PRIOR APPLICATION NUMBER: 60/131270
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131272
PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-04-27
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PRIOR FILING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: 60/138166
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/144791
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 60/146970
PRIOR FILING DATE: 1999-08-03
PRIOR APPLICATION NUMBER: 60/162506
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/311832
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/380142
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/44848
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/747259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/816744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/854208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/854280

PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 09/874503
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: 09/869599
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/908,827
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US99/10723
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: PCT/US99/28551
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30720
PRIOR FILING DATE: 1999-12-22
PRIOR APPLICATION NUMBER: PCT/US00/05601
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 80
SEQ ID NO 67
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-035-977-67

Query Match 99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWIILVLPVLPQAFPKPGSGQDSLSHNRLESAERPLNEQIAEAEDKIKKTYPP 60
DB 1 MGFLGTGWIILVLPVLPQAFPKPGSGQDSLSHNRLESAERPLNEQIAEAEDKIKKTYPP 60
QY 61 ENKPGQSYNSFYDNLNLRAITEKEKIERQSSIRSSPLDNKLNEVDSTKRNRLIDY 120
DB 61 ENKPGQSYNSFYDNLNLRAITEKEKIERQSSIRSSPLDNKLNEVDSTKRNRLIDY 120
QY 121 DSTKSGLHKFPDDPDGHLQDGLTPLTADYHKAARIYEENDRAVFDKIVSKLNLGL 180
DB 121 DSTKSGLHKFPDDPDGHLQDGLTPLTADYHKAARIYEENDRAVFDKIVSKLNLGL 180
QY 181 ITESQAHLEDEVAEVLQKLSKEANNNEEDPNKPTSWTENQAGKIPKVTYPMMAIQDGL 240
DB 181 ITESQAHLEDEVAEVLQKLSKEANNNEEDPNKPTSWTENQAGKIPKVTYPMMAIQDGL 240
QY 241 AKGENDEVSNLTITLNGLERRTKTYSEDNFRDFOYFPNFYALLKLSISSEKAEKETLI 300
DB 241 AKGENDEVSNLTITLNGLERRTKTYSEDNFRDFOYFPNFYALLKLSISSEKAEKETLI 300
QY 301 TIMKTLIDFVKMMVYGTISPEGVSYLENDEMIATQKKNLEKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVYGTISPEGVSYLENDEMIATQKKNLEKNATDNISKLPAPSE 360

```
OY 361 KSHETDSTKEAAKMEKEYSLKSTKDNNSPGKTEDEPKTEAYLEAIRKNIEWLK 420
|||
Db 361 KSHETDSTKEAAKMEKEYSLKSTKDNNSPGKTEDEPKTEAYLEAIRKNIEWLK 420
OY 421 KHDKGKNEKEDYDLKSKMRDPIKNOADAYVEKGIIDKEEAFAIKRIYSSL 468
|||
Db 421 KHDKGKNEKEDYDLKSKMRDPIKNOADAYVEKGIIDKEEAFAIKRIYSSL 468
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RESULT 3

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US-10-063-735-150
; Sequence 150, Application US/10063735
; Publication No. US20030138882A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William T.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,735
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 150
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-735-150
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Query Match 99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OY 1 MGFLGTGWTILVLPPIQAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
|||
Db 1 MGFLGTGWTILVLPPIQAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
OY 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVDSTKNRKLIDY 120
|||
Db 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVDSTKNRKLIDY 120
OY 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNLGL 180
|||
Db 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNLGL 180
OY 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAA10DGL 240
|||
Db 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAA10DGL 240
OY 241 AKGENDETVSNLTLTNGLERTKTYSEDNFELOYPFNFYALLKSIDSEKAEKETLI 300
|||
Db 241 AKGENDETVSNLTLTNGLERTKTYSEDNFELOYPFNFYALLKSIDSEKAEKETLI 300
OY 301 TIMKTLIDFVKMVKYGTISPEGVSYLENIDEMIALQTKNKLKKNATONISKLFPAPSE 360
|||
Db 301 TIMKTLIDFVKMVKYGTISPEGVSYLENIDEMIALQTKNKLKKNATONISKLFPAPSE 360
OY 361 KSHETDSTKEAAKMEKEYSLKSTKDNNSPGKTEDEPKTEAYLEAIRKNIEWLK 420
|||
Db 361 KSHETDSTKEAAKMEKEYSLKSTKDNNSPGKTEDEPKTEAYLEAIRKNIEWLK 420
OY 421 KHDKGKNEKEDYDLKSKMRDPIKNOADAYVEKGIIDKEEAFAIKRIYSSL 468
|||
Db 421 KHDKGKNEKEDYDLKSKMRDPIKNOADAYVEKGIIDKEEAFAIKRIYSSL 468
```

RESULT 4

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US-10-137-870-90
; Sequence 90, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Laureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-90
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Query Match 99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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OY 1 MGFLGTGWTILVLPPIQAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
|||
Db 1 MGFLGTGWTILVLPPIQAFPKPGSQDSSLNRELASRPINQIAEAEDKIKKTYPP 60
OY 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVDSTKNRKLIDY 120
|||
Db 61 ENKPGQSNYSFVDNLNLKAITTEKEKIEKERSIRSSPLDNKLNVEDVDSTKNRKLIDY 120
OY 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNLGL 180
|||
Db 121 DSTKSGLDHKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNLGL 180
OY 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAA10DGL 240
|||
Db 181 ITESQAHTLEDEVAEYLOKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAA10DGL 240
OY 241 AKGENDETVSNLTLTNGLERTKTYSEDNFELOYPFNFYALLKSIDSEKAEKETLI 300
|||
Db 241 AKGENDETVSNLTLTNGLERTKTYSEDNFELOYPFNFYALLKSIDSEKAEKETLI 300
OY 301 TIMKTLIDFVKMVKYGTISPEGVSYLENIDEMIALQTKNKLKKNATONISKLFPAPSE 360
|||
Db 301 TIMKTLIDFVKMVKYGTISPEGVSYLENIDEMIALQTKNKLKKNATONISKLFPAPSE 360
OY 361 KSHETDSTKEAAKMEKEYSLKSTKDNNSPGKTEDEPKTEAYLEAIRKNIEWLK 420
|||
Db 361 KSHETDSTKEAAKMEKEYSLKSTKDNNSPGKTEDEPKTEAYLEAIRKNIEWLK 420
OY 421 KHDKGKNEKEDYDLKSKMRDPIKNOADAYVEKGIIDKEEAFAIKRIYSSL 468
|||
Db 421 KHDKGKNEKEDYDLKSKMRDPIKNOADAYVEKGIIDKEEAFAIKRIYSSL 468
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Sequence 90, Application US/10140274
Publication No. US20030143674A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C163
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 90
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-274-90
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Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWLIVLVLPPIQAFPPKPGSODKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWLIVLVLPPIQAFPPKPGSODKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVNDNLNLRATTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVNDNLNLRATTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
QY 121 DSTSGDLHKFQDDPDGLHQLDGTPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
DB 121 DSTSGDLHKFQDDPDGLHQLDGTPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
QY 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDPNKPTSWENQAGKIPKVTYPMMAIQQDGL 240
DB 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDPNKPTSWENQAGKIPKVTYPMMAIQQDGL 240
QY 241 AKGENDETYSNTLTLNGLERRRTKYSSEDFRFOYFPNPFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETYSNTLTLNGLERRRTKYSSEDFRFOYFPNPFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEVGS�KDSKDNNSNPGGKTDEPKGTETAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEVGS�KDSKDNNSNPGGKTDEPKGTETAYLEAIRKNIEWLK 420
QY 421 KHKKGKNEKEDYDLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
DB 421 KHKKGKNEKEDYDLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
```

```
RESULT 8
US-10-140-471-90
Sequence 90, Application US/10140471
```

```
Publication No. US20030138887A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C163
CURRENT APPLICATION NUMBER: US/10/140,471
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 90
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-471-90
```

```
Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWLIVLVLPPIQAFPPKPGSODKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWLIVLVLPPIQAFPPKPGSODKSLHNRELSAERPLNEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVNDNLNLRATTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVNDNLNLRATTEKEKTEKROSTIRSSPLDNKLNEVDVSTKNRKLIDY 120
QY 121 DSTSGDLHKFQDDPDGLHQLDGTPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
DB 121 DSTSGDLHKFQDDPDGLHQLDGTPLTAEDIVHKIARIYEENDRAVFDKIVSKLNLGL 180
QY 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDPNKPTSWENQAGKIPKVTYPMMAIQQDGL 240
DB 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDPNKPTSWENQAGKIPKVTYPMMAIQQDGL 240
QY 241 AKGENDETYSNTLTLNGLERRRTKYSSEDFRFOYFPNPFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETYSNTLTLNGLERRRTKYSSEDFRFOYFPNPFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFYKMMVKYGTISPPEGVSYLENLDEMIALQTKNKLKKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEVGS�KDSKDNNSNPGGKTDEPKGTETAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEVGS�KDSKDNNSNPGGKTDEPKGTETAYLEAIRKNIEWLK 420
QY 421 KHKKGKNEKEDYDLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
DB 421 KHKKGKNEKEDYDLSKMRDFTNKQADAYVEKGIIDKEEAFAIKRIYSSL 468
```

```
RESULT 9
US-10-140-807-90
Sequence 90, Application US/10140807
Publication No. US20030134354A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC174
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-90

```

```

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWIIVLVLPVLPQAFPPKPGSGQDSLSHNRELASRPPLNEQJAEAEEDKIKKITYPP 60
DB 1 MGFLGTGWIIVLVLPVLPQAFPPKPGSGQDSLSHNRELASRPPLNEQJAEAEEDKIKKITYPP 60
QY 61 ENKPGQSNYSFVDNMLNLRAITEKEKIEKERSIRSSPLDNKLNVEDVSTNRKRLIDY 120
DB 61 ENKPGQSNYSFVDNMLNLRAITEKEKIEKERSIRSSPLDNKLNVEDVSTNRKRLIDY 120
QY 121 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
DB 121 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
QY 122 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
DB 122 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
QY 181 ITESQAHNLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTPEMAAIQDGL 240
DB 181 ITESQAHNLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTPEMAAIQDGL 240
QY 241 AKGENDETVSNLTTLNGLERRTKTYSEDNFELOYFPNRYALLKSIDSEKAKEKETLI 300
DB 241 AKGENDETVSNLTTLNGLERRTKTYSEDNFELOYFPNRYALLKSIDSEKAKEKETLI 300
QY 301 TIMKTLIDFVKMMVYKGTISPREGVSYLENLDEMIALQTKNLEKKNATNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVYKGTISPREGVSYLENLDEMIALQTKNLEKKNATNISKLPAPSE 360
QY 361 KSHETDSTKEEAAMKEKEGSLKSDTKDONSNGKTEDEPKGTPEAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAMKEKEGSLKSDTKDONSNGKTEDEPKGTPEAYLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLSKMRDFINQADAYVEKGILDKKEEAIAIRIYSSL 468
DB 421 KHKDKGNKEDYDLSKMRDFINQADAYVEKGILDKKEEAIAIRIYSSL 468

```

```

RESULT 10
US-10-140-922-90
; Sequence 90, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC179
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-922-90

```

```

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWIIVLVLPVLPQAFPPKPGSGQDSLSHNRELASRPPLNEQJAEAEEDKIKKITYPP 60
DB 1 MGFLGTGWIIVLVLPVLPQAFPPKPGSGQDSLSHNRELASRPPLNEQJAEAEEDKIKKITYPP 60
QY 61 ENKPGQSNYSFVDNMLNLRAITEKEKIEKERSIRSSPLDNKLNVEDVSTNRKRLIDY 120
DB 61 ENKPGQSNYSFVDNMLNLRAITEKEKIEKERSIRSSPLDNKLNVEDVSTNRKRLIDY 120
QY 121 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
DB 121 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
QY 122 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
DB 122 DSTKSGLDHKKFODDDPGHQLDGTPLTADIVHAKIARIYEENDRAVFPDKIVSKLLNLGL 180
QY 181 ITESQAHNLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTPEMAAIQDGL 240
DB 181 ITESQAHNLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTPEMAAIQDGL 240
QY 241 AKGENDETVSNLTTLNGLERRTKTYSEDNFELOYFPNRYALLKSIDSEKAKEKETLI 300
DB 241 AKGENDETVSNLTTLNGLERRTKTYSEDNFELOYFPNRYALLKSIDSEKAKEKETLI 300
QY 301 TIMKTLIDFVKMMVYKGTISPREGVSYLENLDEMIALQTKNLEKKNATNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVYKGTISPREGVSYLENLDEMIALQTKNLEKKNATNISKLPAPSE 360
QY 361 KSHETDSTKEEAAMKEKEGSLKSDTKDONSNGKTEDEPKGTPEAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAMKEKEGSLKSDTKDONSNGKTEDEPKGTPEAYLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLSKMRDFINQADAYVEKGILDKKEEAIAIRIYSSL 468
DB 421 KHKDKGNKEDYDLSKMRDFINQADAYVEKGILDKKEEAIAIRIYSSL 468

```

```

RESULT 11
US-10-140-924-90
; Sequence 90, Application US/10140924
; Publication No. US2003013435A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

```

```

; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC17
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-924-90

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 MGFLGTGWIIVLVLPIDQAPPPGSGQSKLNHRELASRPLEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWIIVLVLPIDQAPPPGSGQSKLNHRELASRPLEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
QY 121 DSTSGGLDHRFQDDPDGHLQDGTPLTADYVHKIARIEENDRAVDFKIVSKLNLGL 180
DB 121 DSTSGGLDHRFQDDPDGHLQDGTPLTADYVHKIARIEENDRAVDFKIVSKLNLGL 180
QY 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
DB 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
QY 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMIALQTKNKLKNKATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMIALQTKNKLKNKATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEVYSLKSDSTKDONSNGPKTDEPKGTEATVLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEVYSLKSDSTKDONSNGPKTDEPKGTEATVLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLKSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
DB 421 KHKDKGNKEDYDLKSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
```

```

RESULT 12
US-10-140-926-90
; Sequence 90, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
```

```

; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC187
; CURRENT APPLICATION NUMBER: US/10/140,926
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-140-926-90

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 MGFLGTGWIIVLVLPIDQAPPPGSGQSKLNHRELASRPLEQIAEAEEDKIKKTYPP 60
DB 1 MGFLGTGWIIVLVLPIDQAPPPGSGQSKLNHRELASRPLEQIAEAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITEKEKIEROSIRSSPLDNKLNVEDVSTKNRKLIDY 120
QY 121 DSTSGGLDHRFQDDPDGHLQDGTPLTADYVHKIARIEENDRAVDFKIVSKLNLGL 180
DB 121 DSTSGGLDHRFQDDPDGHLQDGTPLTADYVHKIARIEENDRAVDFKIVSKLNLGL 180
QY 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
DB 181 ITESQAHTEDEVAEVLQKLSKEANNYEEDNPKPTSWENQAGKIPKVTMPAAIÖDGL 240
QY 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETYSNTLTLTNGLERRTKTYSEDNFRDFOYFPNFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMIALQTKNKLKNKATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMMVKYGTISPEEGVSYLENDEMIALQTKNKLKNKATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAKMEKEVYSLKSDSTKDONSNGPKTDEPKGTEATVLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAKMEKEVYSLKSDSTKDONSNGPKTDEPKGTEATVLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDYDLKSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
DB 421 KHKDKGNKEDYDLKSKMRDFINKQADAYVEKGIIDKEEAIAIKRIYSSL 468
```

```

RESULT 13
US-10-141-698-90
; Sequence 90, Application US/10141698
; Publication No. US20030134357A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
```

```

; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC206
; CURRENT APPLICATION NUMBER: US/10/141,698
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-698-90

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 MGFLGTGWILVLPPIQAFPRKGGSDKSLHNRLSARPLNEQIAEEDKIKKTYPP 60
DB 1 MGFLGTGWILVLPPIQAFPRKGGSDKSLHNRLSARPLNEQIAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNINLRAITEKEKIEKERSISSPLDNKLNVEDVSTNRKLIIDY 120
DB 61 ENKPGQSNYSFVDNINLRAITEKEKIEKERSISSPLDNKLNVEDVSTNRKLIIDY 120
QY 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
DB 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
QY 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
DB 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
QY 181 ITESQAHNLEDEVAEVLQKLISKANNEYEDNPKPTSWENQAGKIPEKVTYMAAIQDGL 240
DB 181 ITESQAHNLEDEVAEVLQKLISKANNEYEDNPKPTSWENQAGKIPEKVTYMAAIQDGL 240
QY 241 AKGNDETVSNLTTLTNGLERRTKTYSEDNFRDFOYFPFVYALKSIDSEKAKEKETLI 300
DB 241 AKGNDETVSNLTTLTNGLERRTKTYSEDNFRDFOYFPFVYALKSIDSEKAKEKETLI 300
QY 301 TIMKTLIDFVKMVKYGTISPEEGVSYLENIDEMIALQTKNLEKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMVKYGTISPEEGVSYLENIDEMIALQTKNLEKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAAMEKEKYGSLKSTKDONSNGPKGTDEPKGTEAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAAMEKEKYGSLKSTKDONSNGPKGTDEPKGTEAYLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDVDLSKMRDPINKQADAYVEKGLIDKEEAIRKRIYSSL 468
DB 421 KHKDKGNKEDVDLSKMRDPINKQADAYVEKGLIDKEEAIRKRIYSSL 468
```

```

RESULT 14
US-10-141-702-90
; Sequence 90, Application US/10141702
; Publication No. US20030134358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
```

```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC208
; CURRENT APPLICATION NUMBER: US/10/141,702
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-141-702-90

Query Match          99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```

QY 1 MGFLGTGWILVLPPIQAFPRKGGSDKSLHNRLSARPLNEQIAEEDKIKKTYPP 60
DB 1 MGFLGTGWILVLPPIQAFPRKGGSDKSLHNRLSARPLNEQIAEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNINLRAITEKEKIEKERSISSPLDNKLNVEDVSTNRKLIIDY 120
DB 61 ENKPGQSNYSFVDNINLRAITEKEKIEKERSISSPLDNKLNVEDVSTNRKLIIDY 120
QY 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
DB 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
QY 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
DB 121 DSTKSGLDHKKFODDPDGLHQLDGTPLTAEDIYHKIAARIYEENDRAVFDKIVSKLLNGL 180
QY 181 ITESQAHNLEDEVAEVLQKLISKANNEYEDNPKPTSWENQAGKIPEKVTYMAAIQDGL 240
DB 181 ITESQAHNLEDEVAEVLQKLISKANNEYEDNPKPTSWENQAGKIPEKVTYMAAIQDGL 240
QY 241 AKGNDETVSNLTTLTNGLERRTKTYSEDNFRDFOYFPFVYALKSIDSEKAKEKETLI 300
DB 241 AKGNDETVSNLTTLTNGLERRTKTYSEDNFRDFOYFPFVYALKSIDSEKAKEKETLI 300
QY 301 TIMKTLIDFVKMVKYGTISPEEGVSYLENIDEMIALQTKNLEKNATDNISKLPAPSE 360
DB 301 TIMKTLIDFVKMVKYGTISPEEGVSYLENIDEMIALQTKNLEKNATDNISKLPAPSE 360
QY 361 KSHETDSTKEEAAAMEKEKYGSLKSTKDONSNGPKGTDEPKGTEAYLEAIRKNIEWLK 420
DB 361 KSHETDSTKEEAAAMEKEKYGSLKSTKDONSNGPKGTDEPKGTEAYLEAIRKNIEWLK 420
QY 421 KHKDKGNKEDVDLSKMRDPINKQADAYVEKGLIDKEEAIRKRIYSSL 468
DB 421 KHKDKGNKEDVDLSKMRDPINKQADAYVEKGLIDKEEAIRKRIYSSL 468
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```

RESULT 15
US-10-141-704-90
; Sequence 90, Application US/10141704
; Publication No. US20030134359A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

APPLICANT: Gao, Wei-Qiang
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C209
CURRENT APPLICATION NUMBER: US/10/141,704
CURRENT FILING DATE: 2002-05-08
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 90
LENGTH: 468
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-704-90

Query Match 99.3%; Score 2384; DB 12; Length 468;
Best Local Similarity 99.1%; Pred. No. 1.2e-152;
Matches 464; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGFLGTGWTWLVLPVPIAFKPGSGQSKLHNRLSAPRLNEQIAFEEDKIKKTYPP 60
DB 1 MGFLGTGWTWLVLPVPIAFKPGSGQSKLHNRLSAPRLNEQIAFEEDKIKKTYPP 60
QY 61 ENKPGQSNYSFVDNLNLRAITTEKEKTEKERSIRSSPLDNKLNVEDVSTKNRRLDDY 120
DB 61 ENKPGQSNYSFVDNLNLRAITTEKEKTEKERSIRSSPLDNKLNVEDVSTKNRRLDDY 120
QY 121 DSTSGLDHKFODDPDGLHQLDGTPLTAEDIVHKIAARIYENDRAVFDKIVSKLNLGL 180
DB 121 DSTSGLDHKFODDPDGLHQLDGTPLTAEDIVHKIAARIYENDRAVFDKIVSKLNLGL 180
QY 181 ITESQAHLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPKVTYPMATIDGL 240
DB 181 ITESQAHLEDEVAEVLQKLSKEANNYEEDPNKPTSWTENQAGKIPKVTYPMATIDGL 240
QY 241 AKGENDETVSNTLTLTNGLERRTKTYSEDNFRDFQYPPNFYALKSIDSEKAEKETLI 300
DB 241 AKGENDETVSNTLTLTNGLERRTKTYSEDNFRDFQYPPNFYALKSIDSEKAEKETLI 300
QY 301 TIMKTLDYFKMMVKYGTISPEEGVSTLENDEMIALQTKNKLKNAATDNISKLEPAPSE 360
DB 301 TIMKTLDYFKMMVKYGTISPEEGVSTLENDEMIALQTKNKLKNAATDNISKLEPAPSE 360
QY 361 KSHETDSTKEEAKMEKEVSLKSDSTKDNNSNGCKTDEPKGTEAYLEAIRNTEMLK 420
DB 361 KSHETDSTKEEAKMEKEVSLKSDSTKDNNSNGCKTDEPKGTEAYLEAIRNTEMLK 420
QY 421 KHKDKGKEDYDLSKMRDFTNKQADAYVEKGIIDKEEPAIKRIYSSL 468
DB 421 KHKDKGKEDYDLSKMRDFTNKQADAYVEKGIIDKEEPAIKRIYSSL 468

Search completed: August 28, 2003, 10:31:55
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 09:59:03 ; Search time 69 Seconds
(without alignments)
1750.270 Million cell updates/sec

Title: US-09-554-945b-2

Perfect score: 2402

Sequence: 1 MGFLGTGWTIVLVLPIDAF.....EKGLDKERAEAKRIYSL 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2053	85.5	466	11	Q81d7 mus musculu
2	1216	50.6	457	13	Q91847 xenopus lae
3	200	8.3	7210	5	Q9v7g8 drosophila
4	200	8.3	9270	5	Q8MID9 Osmid9 drosophila
5	197	8.2	2081	10	Q9LH98 O9LH98 arabidopsis
6	191	8.0	2139	5	Q07569 entamoeba h
7	188.5	7.8	2760	5	Q815Y2 O815Y2 plasmodium
8	187.5	7.8	1661	5	Q06166 plasmodium
9	183.5	7.6	1175	16	O8XNw6 plasmodium
10	183	7.6	1434	5	O81492 plasmodium
11	182	7.6	951	5	O96229 plasmodium
12	181	7.5	1790	5	Q07380 saccharomyc
13	180.5	7.5	3504	5	O81L45 plasmodium
14	180	7.5	1871	10	O9SRD5 O9SRD5 arabidopsis
15	179.5	7.5	853	10	O9LFE4 O9LFE4 arabidopsis
16	178.5	7.4	1263	5	O81K49 plasmodium

17	178.5	7.4	1964	5	O85W07	O85W07 lolligo peal
18	177.5	7.4	682	5	O81BV6	O81BV6 plasmodium
19	175	7.3	10578	5	O81SE5	O81SE5 caenorhabdi
20	175	7.3	18519	5	O81SE6	O81SE6 caenorhabdi
21	175	7.3	18534	5	O81SE7	O81SE7 caenorhabdi
22	174.5	7.3	1320	11	O9JK25	O9JK25 rattus norv
23	174.5	7.3	1323	5	O9NB35	O9NB35 plasmodium
24	174.5	7.3	1510	5	O25920	O25920 plasmodium
25	173	7.2	1358	5	O96275	O96275 plasmodium
26	173	7.2	1786	5	O9U0P0	O9U0P0 plasmodium
27	172.5	7.2	1979	5	O96133	O96133 plasmodium
28	172	7.2	493	5	O25886	O25886 plasmodium
29	171.5	7.1	1795	5	O81E35	O81E35 plasmodium
30	171.5	7.1	2612	5	O815X5	O815X5 plasmodium
31	171	7.1	734	5	O95V49	O95V49 drosophila
32	171	7.1	840	5	O815X4	O815X4 plasmodium
33	171	7.1	2269	5	O26223	O26223 plasmodium
34	171	7.1	2747	5	O9BUX9	O9BUX9 plasmodium
35	170.5	7.1	1596	5	O81J44	O81J44 plasmodium
36	169.5	7.1	1134	2	O99051	O99051 streptococ
37	169.5	7.1	1464	5	O81IF6	O81IF6 plasmodium
38	169	7.0	1909	5	O25893	O25893 plasmodium
39	169	7.0	3484	5	P91257	P91257 caenorhabdi
40	168	7.0	1272	16	O98PR8	O98PR8 mycoplasma
41	168	7.0	2006	5	O81D10	O81D10 plasmodium
42	168	7.0	2867	5	O9N2M3	O9N2M3 plasmodium
43	167.5	7.0	924	5	O15738	O15738 dictyosteli
44	167	7.0	1112	16	O8EMQ1	O8EMQ1 mycoplasma
45	167	7.0	2771	5	O26216	O26216 plasmodium

ALIGNMENTS

RESULT 1
ID O81D7 PRELIMINARY: PRT: 466 AA.

AC O81D7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Similar to secretograin III.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SOURCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024785; AAH24785.1;
SQ SEQUENCE 466 AA; 52783 MW; ABLCB9667276315C CRC64;

Query Match 85.5%; Score 2053; DB 11; Length 466;
Best Local Similarity 86.6%; Pred. No. 5,8e-96;
Matches 408; Conservative 17; Mismatches 38; Indels. 8; Gaps 2;

QY	1	MGFLGTGWTIVLVLPIDAFPPKPGSODKSLHNRELSAERPLNEQJAEAEEDIKRT	57
DB	1	MGFLGTGWTIVLVLPIDAFPPKPGSODKSLHNRELSAERPLNEQJAEAEADIKKA	60
QY	58	YPPENKPGQSNYSFVNLNLRAITEKEKEKERQSIKSSPLDNKLNVEDVSTKRRKI	117
DB	61	FPEESKPSSESNYSVNLNLRAITEKEKEKERQSIKSSPLDNKLNVEDVSTKRRKI	120
QY	118	DDYDSTKSGIDHKFGDDPGDLHLDGTPLAEDIVKIAARIYEENDRAVDFKYSKLN	177
DB	121	DEYDSTKSGIDHKFGDDPGDLHLDGTPLAEDIVKIAARIYEENDRAVDFKYSKLN	180
QY	178	LGITTSQAHTLEDEVAEALQKLSKEANNYEEDPKPSWMPENOGKIPKVTYPAALIO	237
DB	181	LGITTSQAHTLEDEVAEALQKLSKEANNYEEDPKPSWMPENOGKIPKVTYPAALIO	240

Db 3_48 PSBDKNADESDSTKEEAKKERREYELLKSTKREPND--AAESKPGRKAATYLEAIRKNIT 405
Qy 417 EWLKKHDKCKNKEDDYDLSKMRDFINKOADAAYVEKGILDKEEAFAIRIVSSYL 468
Db 406 EWLKEHNKNEANKGDNLSKLKPFVMOQAADSYVEKGILDKEEANWIKRIVSSYL 457

RESULT 3

ID Q9V7G8 PRELIMINARY; PRT; 7210 AA.

AC Q9V7G8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, last annotation update)
DE CG18255 protein.
GN STRN-mLCK OR CG8304 OR CG18255.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
OX NCBI_TaxID=71227;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goebye J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blakej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Adayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhattacharya D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burdick K.C., Busam D.A., Butler H., Brocktein P., Brodtier P.,
RA Cherry J.M., Cavley S., Dahlke C., Davernport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Meyers A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Flosser C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
RA Glisdek A., Gong F., Gorrell T.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Huston K.A., Howland T.J., Wei M.-H., Ikegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klupp D., Lal Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J.Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusseren D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Relentst K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shne B.C., Sidan-Kimos I., Simpson M., Skupski M.P., Smith T.,
RA Splter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svistkas R., Tecator C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zavertl J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Sequence 287:2185-2195(2000).

[2]

RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Goebye J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Barzon J., An H., Baldwin D., Barzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dorson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galie R.F., Gang N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ikegawa C., Jalali M., Kruse D., Li P., Matelli B., Mochizuki T.,
RA Paoletti M., Peterson J., Platt R., Rothberg L., Samadpour M.,
RA Scheeler F., Shen H., Simpson M., Skupski M.P., Smith T.,
RA Stapp J., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svistkas R., Tecator C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zavertl J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."

RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Bertram B., Carlson J.W., Celinker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak P., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 DR EMBL: AB003808; AAM70936.1; -;
 DR Flybase: FBgn0013988; Strn-M1Ck.
 DR InterPro: IPR003961; FN-III.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig-C2.
 DR InterPro: IPR003006; Ig-MHC.
 DR InterPro: IPR003596; Ig-V.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr-kinase.
 DR InterPro: IPR001245; Tyr-kinase.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 29.
 DR Pfam: PF00069; pkinase; 1.
 DR Prodom: PD000001; Prot_kinase; 1.
 DR SMART: SM00408; Igc2; 29.
 DR SMART: SM00406; Igv; 4.
 DR SMART: SM00220; S-TC; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS50835; IG_LIKE; 26.
 DR PROSITE: PS00290; IG_MHC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding: Immunoglobulin domain; Transferase.
 KW SEQUENCE 9270 AA; 1036749 MW; 0DD82D040B27C2AD CRC64;
 SQ
 Query Match 8.3%; Score 200; DB 5; Length 9270;
 Best Local Similarity 23.8%; Pred. No. 0.42;
 Matches 110; Conservative 83; Mismatches 180; Indels 90; Gaps 19;
 QY 35 ELASERPLNEQIAEEDKIKKTYPPENKPGOSNYSFVONLNLRAITEKEIEKEROSI 94
 DB 4757 EIVSEKITDEKAQESQKEVGS---EAKPKAKV-----LEKKSIEEKLKKKEQ 4806
 QY 95 RSPSLDNKLVNEDVSTNRRLLID--YDSTKSGIDHKFODDPDGLHOLDGTPLTAEIDV 152
 DB 4807 TESAIIDKESQAKAEVSEIYSEKITDEKAQESQKEVGS-EAKPKAKVLEKKSIEEKL 4865
 QY 153 HK-----IAARIYENDRAVDFPKIYSKLNLGLITESQAHTEDEVAEVLQ-KLISKEANN 207
 DB 4866 NKKKQTESAIIDKESQAKAEVSEIYSEKITDEKAQESQKEVGS-EAKPKAKVLEKKSIE 4925
 QY 208 YEEDPNKPTSWTENQAGKIPKAVPMAIIOGLAKGDETVSNLTLTNGLEERTKTYIS 267
 DB 4926 EEKEDKKKEKTE-----SAIDKFKQAEVSEIYSEKIT-----DEKAESR 4967
 QY 268 EDNFRDFOYFPNFYALF--KSIDSEK--EAKKET-----LITIMKTLID-- 308
 DB 4968 KEEVKDSEAKPKKAKVLEKKSIEEKLKKKEKQTESAIIDKESQAKAEVSEIYSEKITDEK 5027

QY 309 ---FVKMKVYKGTISP-----EEGVSYLENLDEMIALQTKNLEKNATNISKLPAPS 359
 DB 5028 AQESQKKEVNDSEAKPKKAKVLEKKSIEEKLDEKKEKQIETKV---ATDKSQVEVSE 5084
 QY 360 EKSIEETDSTKEEAKMEKEVSLKSDTSDNSNPGKTDPEKGTAEVLEAIRKNIEML 419
 DB 5085 IYLEKISIEEKAEEQAKVE-----LKDS-----EAKSKAKVLEKKSITLKEKL 5126
 QY 420 KKHKKKKKKEDYDLSKKRDFINKQADAVKEGILDKKEAEAIK 462
 DB 5127 DENDKK-QKEGATNKSQK--AEADAVPEK--ISEEKVAEIK 5164
 RESULT 5
 Q9LH98 PRELIMINARY; PRT; 2081 AA.
 ID Q9LH98
 AC Q9LH98;
 DT 01-OCN-2000 (TREMBlrel, 15, Created)
 DT 01-OCN-2000 (TREMBlrel, 15, Last sequence update)
 DT 01-OCN-2002 (TREMBlrel, 22, Last annotation update)
 DE Genomic DNA, chromosome 3, BAC clone: T19N8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-Columbia;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Columbia;
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by miniseq p1,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 DR EMBL: AP002057; BAB03174.1; -;
 DR EMBL: AP002057; BAB03174.1; -;
 SQ SEQUENCE 2081 AA; 232851 MW; D3603E1F85EFF729 CRC64;
 SQ
 Query Match 8.2%; Score 197; DB 10; Length 2081;
 Best Local Similarity 25.2%; Pred. No. 0.1;
 Matches 120; Conservative 68; Mismatches 175; Indels 114; Gaps 21;
 QY 27 QKSLHNRPLSARPLNEQIAEED-----KIKKTYPPENKPGOSNYS 70
 DB 707 EDKLEENKESQYDSKDDSVDDKQEBQAIYGESKDDKSVKAKKKESKENKTKTNEN 766
 QY 71 FVDNL--NLRAITEKEKTEK--EROSTISSPLDNKLVNEDVSTNRRLLIDYDSTKSG 126
 DB 767 RVRNKEENVQKKKSEKKEKESKDAKSVETKDN-KKLSSTENR---DEAKERSG 821
 QY 127 IDHKFODDPDGLHOLDGTPLTAEIDVHKIARIYEEN--DRAVEDKIVSKLNLGLITE 183
 DB 822 EDNKEDKESKDYQ-----SVEAKENKNGVDVNGVKGKESKDLKDRSYE 868
 QY 184 SOAHLEED-----EVAEVLQKLSKE---ANNYEDPNKPTSWTENQAGKIPKAVPMA 234
 DB 869 VYANKKESSKKKKEEVORNDKSTKEVRDFANNMIDYQKSGS--ESVYKKRDEK----- 921
 QY 235 AIODGLAGKEDTVSNLTLTNGLEERTKTYISSEDFNFOYFPNFYALLKSIDSEKAK 294
 DB 922 --KEG-NKEENKDTI--NTSSKQKQDKKKKKESKN-----SNMKKEED 962
 QY 295 EKETLITIMKTLIDFVKMKVYKGTISP-----EEGVSYLENLDEMIALQTKNLEKNATNISK 354
 DB 963 KKEYVNNELKQEDKKKETTSSENSKLE---ENKD-----NKKKESDSASAK- 1008
 QY 355 FPAPEKSHLEETDS--TKEEAAKMEKEVSLKSDTSDNSNPG-----GKIDE 400

DB 1009 --NREKXEKSKTKBEAKKESKKSODKKREKDEBEKSKKEKESRDLAKKKEE 1066
QY 401 PKGTAEATLEARKNIEMWKHKHKKNDYDLSKMRDIFINQAOAYVEKGLDKRE 457
DB 1067 TEKKES-----ENHKSKKKEDKKEHDKSKMKKEED--KKEKKHESKSKRKEE 1115

RESULT 6

007569 PRELIMINARY: PRT: 2139 AA.

AC 007569; 002504;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Myosin heavy chain.
GN MYCA.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HMI:IMSS;
RX MEDLINE=93295430; PubMed=8515774;
RA Raymond-Denise A., Sansonetti P., Guillen N.;
RT "Identification and characterization of a myosin heavy chain gene
(mhca) from the human parasitic pathogen Entamoeba histolytica";
RL Mol. Biochem. Parasitol. 59:123-131(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-HMI:IMSS;
RX STRAIN-HMI:IMSS;
RA Guillen N.;
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: L03534; AAB48065.1; -
DR HSSP: P08799; 1MDN.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00612; IQ_2.
DR Pfam: PF00063; myosin_head; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00242; MYSC; 1.
SQ SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 8.0%; Score 191; DB 5; Length 2139;
Best Local Similarity 20.8%; Pred. No. 0.21;
Matches 106; Conservative 107; Mismatches 193; Indels 104; Gaps 23;

QY 20 FPKPGSODKSLHRELAEPRPLNEQIAEEDKIKTKYPPEN-----KFGQSNYSFV 72
DB 85 FEEBGRKKDKLEID-----LKKKLA-----EIKKRAENALASATAKGELEAKIQ 906
QY 73 D-----NNLRAITEKEKIEKERSIRSSPLDKLNVEDVD- 109
DB 907 DLEDKISELESKLSAELDKQELNKEIENLEEDKEKELTIDNKLKDLKSGEDLEY 966
QY 110 -----STKNRLIDYDSTKSGLOHKFPDDPDGLHQLDGTPLTADYHKTIARLY 160
DB 967 EITELNSQINTLN-ATVDRKDKTIAEMOESIDEKEDETIKLGDIKLEEKDDT----- 1020
QY 161 EENDR-----AVPDKIVSKLNLGLITESQAHLDEVAEVAEVLQKLSKANNYEEDPNKPT 216
DB 1021 -EQDADYASATKDDJLAKKLNKTTI-----ECEDAKDEIAKLEOLEDEE--NNKKDLTNEL 1073
QY 217 SKTENQAGKIPKVTYPMAL-----ODGLAKG--ENDETVSNLTTLTG--LERRTKYVS 267
DB 1074 QOTQKLGTEKTESLAQVATKASDERPPLSQNLNENKLTTKNLTKTAKDLKISGLK 1133
QY 268 EENFDEFOYFPFYALKSID-----SEKAEKEKELLITIMKTLIDFV--KMWVKYGTISP 321
DB 1134 QD-YEDLEDDK-----KTBGDLRNAOKIKELDELDTKGADVSOYLOKKEEY----- 1181
QY 322 EBGVSLNLEMDIMALQTKNLEKNAVDNISLFPAPSEKSEETDSTEEAK-----ME 377

DB 1182 ESQIAKQOEKEKAIGNDVKNK-EKTIKE--KELEIOSLQEKIDETFEVEKEDAKKKKEIE 1238
QY 378 KEYSLSKSDTKDONSFGKTEDEPKGTATYLEARKNIEMWKHKHKKNDYDLSKMRDIFINQAOAYVEKGLDKRE 457
DB 1239 KEMKALQOE-KENVESSKSTKDKKKRLDNDKQKLDMDTADNEKLAKARQLEAQL 1297
QY 437 RDEINKQADAYVEKGLDKREAEARKIYRS 466
DB 1298 NEYODNHEKAVADAEILNKKKAOSDKELNS 1327

RESULT 7

0815Y2 PRELIMINARY: PRT: 2760 AA.

AC 0815Y2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
GN PFL0315C.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow J., Sub B., Peterson J., Angioli S.,
RA Perlea M., Allen J., Selengut J., Haft D., Mather M.W., Valdivia A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium falciparum";
RL Nature 419:498-511(2002).
DR EMBL: AE014845; AAN36152.1; -
DR Hypothetical protein.
SQ SEQUENCE 2760 AA; 330896 MW; EE9964C4845181AC CRC64;

Query Match 7.8%; Score 188.5; DB 5; Length 2760;
Best Local Similarity 20.7%; Pred. No. 0.38;
Matches 119; Conservative 97; Mismatches 203; Indels 155; Gaps 24;

QY 29 KSLHRELAEPRPLNEQIAEEDKIKTKYPPEN-----DKIKTYPPENKPGQSNYSFV 73
DB 1452 KNEAKEEETERNINDQVNEKEMDVNSKNEKEIYOVHNEINTNNKEEGKKKLLK 1511
QY 74 NNL--LLRAITEKEKIEKERO--SIRSSPLDKLNVEDYSTKNRLIDYDSTKSGLDH 129
DB 1512 EINDCLNDYINQKKKKKKNNMAMYGRIYKRONNRNINIKNDLKLYSKSESGENDY 1571
QY 130 KF-----QDDPGLHQLDGTPLTA--DIVH-----KIARIYEEN-- 163
DB 1572 AFYAERFEFVITGYNSEPDYLSIDNOAKNEKNKDIHNNNIKISKMKKENTYENSPF 1631
QY 164 ---DRAVPD-----KIVSKLNLGLITESQ----- 186
DB 1632 HNYGRIRYKSKSNPNYNNYKIKSTYHNALKKRKKTKLKSISNSFTMNSNNKIYKR 1691
QY 187 -----HTLEDEVAEVLQKLSKANNYEDP-----NKPTSWTENQAK 225
DB 1692 TSIKNNTIDYNNSTIKTIHKQN--VEDQGYIDLKTRKRLIYDALDINOOTOOKNLK 1749
QY 226 IPEKTYPMALQDGLAKGENDETVSNLTTLTG--LERRTKYSEDNFPDPYFPNFPAL 283
DB 1750 ITENTT-----OVGKKHGN-----VSNITKNTGAMLEKTKRGNNDNEED-----QFSEE 1796
QY 284 LKSIDSEKAEKELITITMKTL-IDFVMMMYKYGTISPSEBQVSLNLEMD----- 334

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Dd      1797  LKALEKLIKLMELNR-IBELTLEBEEKKRLLELSLKVBEKKKKMMBEMKKMEBK 1855
OY      335  IALOTKNKLE-----NATONISKU-----EPAPSKSHETS7KEBAAM--EKE 379
Dd      1856  IELORKEEEKILOYSROEQIRKLELKKKEELKLLENNKLEBQORRREIKKMEBKE 1915
OY      380  YGSLKSDTKDDNSNPGGTDEPRKGTAYL-----EATKNTE--WLKKNDRKGNKED 430
Dd      1916  REKLTAKTEQOKKEEMKKEBQORRKEQOKLMEEMRKFEEOKKVLEKWLBEKKRKLELK 1975
OY      431  YDLSMRDFTINQADAYENGILKEEAEALRI 464
Dd      1976  LEBOKRRE-ERKKMEBEEKKKEEKKEEELIKM 2008

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[illegible]

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Db      1057 VKENEVEKKEEVEKKEE-----VKEEVEKEDT-----1086

QY      256 TNGLEERTKTYSEDNFRDEQYFPMFVALLKSIDSEKAEKET---LITIMKTLLIDFVK 311
      1087 ---ESKDKEIEOE-----KKEEVEKVEKEDTENKOKVIGETIIIEBK 1127

QY      312 MMVKYGTISPESGYSLENDIDEMALDTKKN-LEKNNTDNTSKLPAPSEKSH-EETDST 369
      1128 KEVKKRV---KKNKNKNENKDNVIOELTMDNDVVEKDTANDKYVIEGEKEEVEKKEEV 1184

Db      370 KEAAKKEKEEYGLKDS-----TKDONSPPGKTIDEPYKGT---EAYLEAIRN 415
      1185 KEKEEVEKEEVEKKEEDTESKDETEOEKEKEEVEKVEKEDTENKDKYIOGETIIIEELKE 1244

QY      416 IE--WLKHKDKGKNKEDYDLSK--NRDPIINQOADYVYKGLDKKEAALAIRI 464
      1245 VKKRYKKRNKNENKDNVIOELTMDNDVNEEDTANKKRYTEOEKEEVEEV 1296

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ID	08XNM6	PRELIMINARY:	PRT:	1175 AA.
AC	08XNM6;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Probable exonuclease.			
GN	SBCC OR CPE0216.			
OS	Clostridium perfringens.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
NC	Clostridium.			
RN	NCBI_TaxID=1502;			
RP	SEQUENCE FROM N.A.			
RX	STRAIN=13 / Type A;			
RX	PubMed=1192842;			
RA	Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,			
RA	Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;			
RT	*Complete genome sequence of Clostridium perfringens, an anaerobic			
RT	flesh-eater.?			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).			
DR	EMBL; AP003185; BAB79922.1; -			
DR	Interpro: IPR003439; ABC transporter.			
KW	Exonuclease: Complete proteome.			
SQ	SEQUENCE 1175 AA; 136878 MW; 766D2366525019C1 CRC64;			
QY	Query Match	7.6%;	Score 183.5;	DB 16; Length 1175;
	Best Local Similarity	21.5%;	Pred. No. 0.25;	
	Matches 112; Conservative	86;	Mismatches 190;	Indels 133; Gaps 21
Dy	29 KSLHNRLSMERPLNEQIAEAEADKIKTKYTPPENKPGQSNVSFVNDL-NLRAITKE-	85		
Dy	256 KEYDKRIEIE-----SLVSSEIKSFKEVEISKNADKVIFFINLEIKLEINKEDLK	311		
Dy	86 -RIEKRQSIIRSSPLDNKLNVEDVSTNRKLLIDYDSTKSGLDHKQDDPDDLLDGG	143		
Dy	312 FSELNKKLELILMBRENNKLKEEETPKKKEELPLRLKKERLLS--QKRDILFQIKA	369		
Dy	144 TPLTAEDIVKRI-----AARIYEENDRAVFQIVSK-----LNLG	179		
Dy	370 DGVKLKEACKIPEDRSKCDTKLNSIEENKRLNELKEERKEELFVHEEFNKNTNSG	429		
Dy	180 LITESQAHLEDEVAEVLQKLI--SKAANNVEDPNKFTSWENOAGKIPKYPYMAIQ	237		
Dy	430 LFLINSYESLDQFNEIKSEVEELKRYIKNLNLEDERSEK-----DLKAVESLSKIR	482		
Dy	238 DGLAK-----GENEYTSNLTLLNGLEKRTKTYSEDNFDFQYFP	278		
Dy	483 DKIESLLEKTPGDSNILEKQIKIGVEYREKLNKKYKEIKNSLESLKTRN-----	531		
Dy	279 NFVALLSIDSEKAEKETLTITIKTLIDVKK-----MVGYGTISPEGVSYL	328		

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Dh 532 NFEKILTEENOKLIEKE--VRELKDYINKVVEELAKLRENIYE-GECCPVCSTHH 588
Qy 329 E-----NIDE-----MIALOTKNKLEKNAIDNISL---FPAPSEK-----SHEETDS 368
Dh 589 ELNKVERKINLEESNEKXTILLESKEEKLIELIEFSKIETATLEVENKRIEELNISIEYGE 648
Qy 369 TKEEAK-MEKEXGSLKSDTSDNSNPGKTDPEKGTKEAYLEAIRNIEMLKHKDGN 427
Dh 649 VNERIKFLPEEFENITLKDRIEENLKK-----ENLEKDEKLK--EKKNN 651
Qy 428 KEDYDISKMDPINKQADAVYVEKGLIDKEEAIRKIRYSL 468
Dh 692 LE-----NIFNKAEVILICEKIVREKEIASKIKELDKEL 724

RESULT 10
ID 081492 PRELIMINARY; PRT; 1434 AA.
AC 081492;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Mature parasite-infected erythrocyte surface antigen (MESA) or
DE PFEMP2.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrett B.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=22255708; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Latke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajadream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrett B.G.;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
RT Nature 419:527-531(2002).
DR EMBL: AL929351; CAD51374.1;
SQ SEQUENCE 1434 AA; 168287 MW; AB0005F9DC26C989 CRC64;
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Query Match 7.6%; Score 183; DB 5; Length 1434;

Best Local Similarity 20.7%; Pred. No. 0.33; Indels 102; Gaps 23;

Matches 99; Conservative 98; Mismatches 180; Indels 102; Gaps 23;

Qy 27 ODKSLNRELISAERPLNEQ-----IAEAEDKIKKTYPPENKPGQSNYSFVNLMLRLAI 81

Dh 501 KDKVLEGEDEKEDKKNDEKDKVLEGEDEKEDK-----EKNQCKAD-KYIGSEKQKEI 554

Qy 82 TEKEKTEKE-----ROSINSSPLDNKLNVEDVSTNRKLLIDYDSTKGLDHRKFD-- 133

Dh 555 --KEVEKRYKKKKKKKKKKGIGKEN--DREGNDKVGPEII--IEVEKEIKROVEDGIG 608

Qy 134 --DPDLHQLDGPRPLAEDIVHKIARIYE--ENDRAVADKIVSKLNLGLITTESAHT 188

Dh 609 ENTEGENDKRVGPEIITEVEKEIKROVEDGIGKPEI--EITTEVEKEE 664

Qy 189 LEDEVAEVLQ-----KLISKEANNYEEDPNKPTSWTENQAGKIPEKVTPMALIDGL 240

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Dh 665 IKKQVEGIGKENDESKDLIGOEIITEVEKESIKENDENK-----DAVIGOEIITEEY 719
Qy 241 AKG--ENDETVSNLTTLTNGLERRTYSEDNFRDPYPPNVALKSIDSEKEAKEKET 298
Dh 720 KEGIKEND-----TENKDKVIGOEIITE-----EVKKEIKOKEKGNKEN 759
Qy 299 LITL-----MKTLLDFVKMVKYKGISPEGV--SYLENLD-----EMALOTKRLK 345
Dh 760 ILEIKDIVIGOEIITEVEKVKVIRK--KVEKGIKENHTESKDVIGOEIITEVEKEIEK 816
Qy 346 NATDNISKLFPAPSEKSHETDSTKEEAAMEKEYSGLKSDTSDNSNPGKTDPEKGT 405
Dh 817 QVEEGIK-----ENDTESKRVKIVIGOEIYK-----DVNEEGENDKVTYKQKRVK- 861
Qy 406 EAYLEAIRKNIEMLKHKDKGNKEDYDLK--NRDPIKQADAVYVEKGLIDKEEAIRK 462
Dh 862 EVKKEVKKKKKKKKKKKRNNKNERKDVIGKIEKEDVNEKDTANKDKIEIQEKEKEEVK 920

RESULT 11
ID 096229 PRELIMINARY; PRT; 951 AA.
AC 096229;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Mature parasite-infected erythrocyte surface antigen (MESA) or
DE PFEMP2.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner M.J., Tetteh H., Carnucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum."
RT Science 282:1126-1132(1998).
[2]
RP SEQUENCE FROM N.A.
RA STRAIN=3D7;
RC MEDLINE=99021743; PubMed=9804551;
RA Gardner M.J., Tetteh H., Carnucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perera M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum."
RT Science 282:1126-1132(1998).
[2]
RP SEQUENCE FROM N.A.
RA STRAIN=3D7;
RC MEDLINE=22255705; PubMed=12368864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlson J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiolini S.,
RA Parida M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carnucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrett B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum."
RT Nature 419:498-511(2002).
DR EMBL: AE001410; AAC71925.2;
KW Hypothetical protein.
SQ SEQUENCE 951 AA; 112486 MW; AC08D89358A84F4F CRC64;
```

Query Match 7.6%; Score 182; DB 5; Length 951;

Best Local Similarity 21.8%; Pred. No. 0.23; Indels 110; Gaps 17;

Matches 103; Conservative 78; Mismatches 181; Indels 110; Gaps 17;

Qy 25 GSDKSLNRELISAERPLNEQIAEAEDKIKKTYPPENKPGQSNYSFVNLMLRLAITK 84

Dh 161 GKODISNSNAE--NRKDVKEGVKELEKKEIKISDHHVEKNKS-----DD 206

Qy 85 EKIEKROSISSPLDNKLN-----VEDVSTNRKLLIDYDSTKSLDHRKFDPPDGLHQ 140

Db 207 HKVEENKSDHKEEKKSDHKEEKKVEEHEDEEDKKEKSENNKKNENDEND 266
QY 141 LDGPTPLAEDIYIKIARIYEENDRAVDFKIVKLLNLGITESQAHTLEDEVAEVLQKI 200
Db 267 EDNDEISDEEDVDVEEDKKNENDIDDDK-----KETDTHLEEEENETIEKE 315
QY 201 IS-KEANNYEEDNPKPTSW-TENQAGRIPEKVT PMAIDGLAKGNDENVSTLTLLTG 258
Db 316 FSDKKKKNKKKOTKKEKSDTEKESKDIEK-----EKSKDKE----- 353
QY 259 LEERTTYSEDNFRDFQYPPNFYALLKSIDSEKAEKETLITIMKTLIDFYKMYKGT 318
Db 354 -KEKSKDKEKKEKDK-----KEKSKDIEKE-KEKDIDIEKESK-DTAKKEKDKD 403
QY 319 ISPEGVSYLENDEIALOTKKNLEKNATDNISKLEPPASEKSH-----E 364
Db 404 IEKESK-----KDKELKKNQNDKKKDDNEK-----KNDKODIHDDNDENDMEETE 452
QY 365 EMDSTKEEAAKME-----KEYGSLKSDTK-DQNSNPGKTDPEKGTAEVLEAI 412
Db 453 ENDEDEDEDEDMENKKKKKNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGN 512
QY 413 RNIEMLKHKHKKGNKEDYDLSKMDP-----INKQADAYVEKGILD 454
Db 513 NENNGEN 564

RESULT 12

007380 PRELIMINARY: PRT: 1790 AA.
AC 007380, P89892;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical 206.5 kDa protein YD058W.
GN USOI OR YD058W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Bloescher H., Brandt P.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; 274106; CAA98621.1;
DR EMBL; 274105; CAA98620.1;
DR SGD; S0002216; USOI.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR006955; USOI_P115_C.
DR InterPro: IPR006953; USOI_P115_C.
DR Pfam; PF04871; USOI_P115_C.1.
DR Pfam; PF04869; USOI_P115_head.1.
SO SEQUENCE 1790 AA; 206450 MW; 90062544f55a52ee CRC64;

Query Match 7.5%; Score 181; DB 3; Length 1790;
Best Local Similarity 19.9%; Pred. No. 0.34;
Matches 118; Conservative 102; Mismatches 16; Indels 196; Gaps 28;

QY 30 SLNRELSEAPRLNEQIAEA--EBDKIKKTPPNKRGOSNYSVDMNLRLATIEKEKI 87
Db 748 SLOETSTHLENLEKLLALNEKELDEKQIILN---SSISLAKENFSIL----- 795
QY 88 EKEQOSIRSSPLDNKLAVEDVSTK---NRKLIDYDSTKSGLDHFKODP---PDGLHQ 140
Db 796 ETELKNVRS-LDMETQLRVLETCKENOTALLEYKST---IHKQEDSIKLTLEKLET 850
QY 141 LDGPTPLAEDIYIKIARIY-----EEN-----DRAVEKIVS 173
Db 851 ILSGKKAADGICINMGDLFALSREMAVEENCKNLQEKDKSVNHNQKETSLEKIDIA 910
QY 174 KLNLGLITES-----QAHTLEDEVAEVLQKLSKEANNYEEDNPKPTSWTENQAGKIP 227

Db 911 KITTEIKAINENLEBKIOCNLSKEKEHISKELVEYKSRFQSHD-----NLVAKLT 961
QY 228 EKVTPMA-----AIODGLAGNDEMYNSLTTLNGLERRTKTYSEDNFRDFO----- 275
Db 962 EKLSLANNYKQMAENESLIIKAVESKNNESSIQLSN-LQNKIDSMQSEK-ENFQIEGNS 1019
QY 276 YPPNFYALLKSIDSEKAEK-----EYLLITIMKTLIDFYKMYKGTISPEGVSYL-- 328
Db 1020 IEKNIELOKLTISDLEOTKEELISKSDSKDEYESQISLKEKLETATANDENVKISE 1079
QY 329 -----ENDPEMIA-----LQKNK-----LEKNAD----- 349
Db 1080 LKTEBELFAELAAKKNLEKLETLETSEKALKEVKNNEHLEKTLQLEKATETKROQ 1139
QY 350 -----NISKLEPPASEKSHEDTST-----KEAAKMEKEX-----GSLKD-----STKDQNS 392
Db 1140 LNSLRANLESL-----EKEHEDLAQOLKKEYEQJANKROQNEELISQINDITSTQONE 1194
QY 393 NPGKTDPEKGTETAY-----LEAIRKNIEMLKHKDKG----- 426
Db 1195 SIKKKNDELVEGVKAMKSTSEQSNLKKSEIDALNLQIKELKKNFTFNASLSEIKSVE 1254
QY 427 -----NKEDYDLSKMDPFIKKAD-----AYVEKGILDKEEAEATK 462
Db 1255 SETYKIKLODECNFKKEKVESELEDKLASEDKNSKITEL-----QKSEKIK 1302

RESULT 13

081145 PRELIMINARY: PRT: 3504 AA.
AC 081145;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Hypothetical protein.
GN Pf14_0404.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=3D7;
RX MEDLINE=22255705; PubMed=1236864;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.-S., Nene V., Shallow S.D., Suh B., Peterson J., Angiuoli S.,
RA Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
RA McPadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
RA Fraser C.M., Barrrell B.,
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum".
RL Nature 419:498-511(2002).
DR EMBL; AE014822; AAN37017.1;
KW Hypothetical protein.
SO SEQUENCE 3504 AA; 408303 MW; B8454D48D55B4F0 CRC64;

Query Match 7.5%; Score 180.5; DB 5; Length 3504;
Best Local Similarity 20.5%; Pred. No. 1.3;
Matches 104; Conservative 93; Mismatches 172; Indels 139; Gaps 22;

QY 32 HN-----RELSAE-----RPLNEQIAEA-----EDKIKKTPPNKRGQ----- 66
Db 982 HNLIGNEVSDERMANEYIISPSEITINDENPTQYEEVSKNINNDKNGKRIINNDOLE 1041
QY 67 ----SNYSFVDMNLRLRAITEKEKIKERQSISSPLDN-----KLNVEDVSTKKNKLTID 118
Db 1042 SPILSNEKKTDDIHI---IEEKEKIDK---PIHNNDLQNEQNHKKIIOQ-----DKLE 1086
QY 119 DYDSTSGLDHFKODPDGLHQDLGPTPLAEDIYIKIARIYEENDRAVDFKIVKLLNL 178


```

Db 1089 EYSLPMSKEK-----NISGONIENLLSNKKEENHKIIHNIIEDPTSK 1134
QY 179 GLITESQAHTLEDEVAEYLOKLISKEANN EEDPNKPTSWEN-----OAKI----- 226
Db 1135 DNEKNMONYIIHDLG---KKDISRENTGEDISPNKYLNKENYGIIDDKKIKIYEENN 1191
QY 227 PEKTPMAAIODGLAKENDETV-----SKYLLTNGLERTRTYSBDN 270
Db 1192 EEEYTDVGSGGNKKSSEGSNDNIMPEYGNKKNSSQENSEDIMEKNGKNSSSEBNDN 1251
QY 271 FRDQYPPNFYALLKSIDSEKEAKEKETLIIMKTLIDFYKMYKGYTISPDEGYSLEN 330
Db 1252 -----IMTEKNGDKKSSEBANONI-----MTEKNGKNKSQO-----N 1285
QY 331 LDEMIALO---TKNKLKNATNDNISKLPAPESEKSHETDST-----KEBAK----- 375
Db 1286 IDDNIMTEKNGKNNSQNSODDNIMTEYEEKNKKSQOETDNIMTEKNGKNKSSEBND 1345
QY 376 --MEKEYGSLDKSDNSNPGGKTDEPKGTETYLEAIRKNIEMLKHKDKGNKEDYDL 433
Db 1346 NIMEKNG--KDKSSEBANONVMT--EKNGKNKSSEBANADNIMTEKNGKNKSSEBND 1402
QY 434 SKMD--FINQADAYVEKGIIDEBAP 459
Db 1403 NIIREGNKKNSSQNSODDNIMTEYEG 1430

```

	RESULT	14
09SRD5		
ID	09SRD5	PRELIMINARY; PRT: 1871 AA.
AC	09SRD5;	
DT	01-MAY-2000 (TREMblrel_13, Created)	
DR	01-MAY-2000 (TREMblrel_13, Last sequence update)	
DY	01-OCT-2002 (TREMblrel_22, last annotation update)	
DE	Putative heat shock protein, 53413-59028.	
OS	F28O16.15.	
OC	Arabidopsis thaliana (Mouse-ear cress).	
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
NCBI_TaxID=3702;	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=cv. Columbia;	
RA	Liu X., Kaul S., Town C.D., Bentio M., Creasy T.H., Haas B.J., Wu D.,	
RM	Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Fraser C.M.;	
RA	Barnstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M.;	
RL	"Submitted (Oct-2000) to the EMBL/Genbank/DBJ databases."	
DR	EMBL; AC010718; AAF0452.1;	
DR	InterPro; IPR002068; HSP20.1.	
DR	PROSITE; PS01031; HSP20.1.	
KW	Heat shock.	
SC	SEQUENCE 1871 AA; 216899 MW; 52300C21F3DBF5A1 CRC64;	
	Query Match	7.5%; Score 180; DB 10; Length 1871;
	Best Local Similarity	20.9%; Pred. No. 0.64;
	Matches 117; Conservative	84; Mismatches 212; Indels 148; Gaps 22;
OY	12 VLVLPTAFKRP--GGSODKSLLNHRELISAEERPLNEQIAEAEDKIRIKTYPPENKPGOSNY 69 : :	: :
Dy	1052 VLVEEETYPDPDKHTGGEDHNDHEEQEKENVAKALEINTEEDSFKEELEKO----- 11050	:
OY	70 SFVGNLNMLIIRAITEKERIEKRROSIIRSSPDLNKLVNVEDYSTKN---RKLDDVDSTKSG 126 : : :	: :
Dy	1106 ---DHGLKSNMVAOKAQETEEK-KTRAMKKNETVERRKOTKGSLGLEGEDPELG 1161	:
OY	127 LDHKFODDPDGILHQLDSTPLN-AEDIVHKITAARIYEENDRAVPD---KVSKTLNLGL 180 : : : : : : :	: :
Dy	1162 --HERRGEDRIELVELTEISDHKEVKYKKDEDYLRSODTGKVDLGERHRNRQRIHK 1219	:
OY	181 ITESQAHTLEDAVENULOKLIISKAN-----NYEEDPNKPVTMTENOAGKIPEKYTP- 232 : : : :	: :

```

Db      1220  SVDEIDIGDDEDAEEAAAVSNENSGSRKQYLTIEEESK-----HKQNKIPBTSNPE 1274
QY      233  -----MAAIDGLAKGEN-----DETASNPLTLNGLERRTKT 265
Db      1275  VNEEDERVEYKETKEVEAHYVLOLEJGKTEKCDKDDGCRERBERGKQMAETMLRQREFT 1334
QY      266  YSEDNFDFQYFPNFAALLKSID--SEKAEKEREYLTITMKLLIDFVKMMKYGTI----- 319
Db      1335  KSDQ-----GIYAKIQTETKEEPPDEKS---QESSHNVKLYVADGSLRNGL 1378
QY      320  ---SPEEGSYLENLEDMALOTKNLEKNATD--NISKLFPAPSEKSHEDST----- 369
Db      1379  EFSEKSEYSTSKMLKLBESKEKEBKHKIRKPTBERSNAPYIEKQGNKKAEEEMQKIDRR 1438
QY      370  -KEEAAKMEKEVGLSD-----STKDDNSNPGKTD-- 399
Db      1439  GKNOELKGOEYGVATLNGEHDKTLEYHNRBEKGTAMENVSSTKIQTQTDLEKRRKRPSEIS 1498
QY      400  -----EPKGTAEVLEAIRKNIEMLKKNHDKKGNKEDYDLS--KKRDFIN 441
Db      1499  ENNHIEFMDSOSODIEEKGSDQAEKRYAKONKIOEVNANDERK--KEEYHISEYRVNEMA 1556
QY      442  K---QADAYVEKGIIDKEAE 459
Db      1557  KRILOVESKANDGSSKKNMETE 1577

```

RESULT 15					
ID	Q9LFE4	PRELIMINARY:	PRT;	853 AA.	
AC	Q9LFE4:				
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DR	01-OCT-2000	(TREMBLrel. 15, Last sequence update)			
DE	01-OCT-2002	(TREMBLrel. 22, Last annotation update)			
GN	Hypothetical protein 96.2 kDa protein.				
OS	F5E19_70.				
OC	Arabidopsis thaliana (Mouse-ear cress).				
CC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
CC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				
CC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.				
CX	NCBI_TaxID=3702;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,				
RA	Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer R.F.X.;				
RL	Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.				
LN	[2]				
RP	SEQUENCE FROM N.A.				
RA	EU Arabidopsis sequencing project;				
RL	Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.				
DR	EMBL: AL391147; CAC01837.1; -				
DR	InterPro: IPR002017; Spectlin.				
DR	SMART: SM00150; SPEC: 1.				
SO	Hypothetical protein.				
SC	SEQUENCE 853 AA; 96207 MW; EB7563AA67F11AAD CRC64;				
Query Match:		7.5%;	Score 179.5;	DB 10;	Length 853;
Best Local Similarity		20.3%;	Pred. No. 0.27;		
Matches 98;		Conservative 82;	Mismatches 209;	Indels 93;	Gaps 17
QY	38 AERPLNEOIAEAEDKIKTKYPENKPKQSINYSFVNDNLNRAT-TEKEKIEKESQIRS	96			
Dd	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :				
Dd	30 AKRFRVNK--SEFSNNNSPSTTTPHRS-----LSLDRSSPNKS SVRRSPKLPT	76			
QY	97 SPLDNKLNVEDVDTSKN-----KKLLDDYDSTSGGLDKHFQDDPDGHLQDGFPLAE	149			
Dd	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :				
QY	77 PPESSQAARVAAYVKGESPOTTTRLSQIREDLKANERISLSLEKDAKALDELKQAQKAEE	136			
Dd	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :				
QY	150 DIHKIRIARIYEENDRAVEFKIVSKLMIGLTSESQAHTLDEVAEVLQKLTIS--KEANN	207			
Dd	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :				
QY	137 QVTILK-----DDL-----KKAKIVEENSELEKQAVAGLIEANYON	173			
Dd	I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :				
QY	208 YEEDPNKPTSWTENQAG-----KIPEKVTPMAAIODGLAK-----	242			

```
Db 174 NEEELKKELETVKNOHSDSALVAVROELEKINEE--LAAAFDAKSKALSOAEDASKT 230
QY 243 ---GENDETVSTLTLITLNGL--ERRKTYSEDNFRDFOYFPNFYALLKSIDSD---EKE 292
Db 231 AETHAEKVDLSSSELTRLKALDSTREKTAISDNEMVAKLEDEIVVLKRDLESARGFEAE 290
QY 293 AKERETLITIMKTLIDFVKMMVYGTISPPEGVSYLENDEMIALOTKKNLEKNAT---D 349
Db 291 VKEKEMIVERKLANDLEAKMAESNAHSLSNEMOSKAKLEEQ--LEEANKLEKSASVSLE 348
QY 350 NICKLEPPAPSEKSH-ETDST--KEEAAMEKEKYGSLKSDTSDNSNPGKTDPEPKYTE 406
Db 349 SVMKOLEGSNDKLDHDETETITDLKERIVTLETTVAQKEDLEVSQRL-GSYEEEYSKNE 407
QY 407 AYDEAIRKNIEMLKHKHDKGNKEDYDLKSKRDFINKQADAYVEKGIIDKEEAIRIYS 466
Db 408 KEVEKLSSELETVKEEKNRAKKEDATSRVORLSEEEKSKLLSDLESSKEEEKSKKAME 467
QY 467 SL 468
Db 468 SL 469
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Search completed: August 28, 2003, 10:23:19
Job time : 72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 10:09:23 ; Search time 44 Seconds
(without alignments)
1022.885 Million cell updates/sec

Title: US-09-554-945b-2

Perfect score: 2402

Sequence: 1 MGFLGTGTWILVLVLPQAF.....EKGILDKREAEAIKRIYSSL 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1942	80.8	533	2 A37180	chromogranin/secre
2	191	8.0	2139	2 T18296	myosin heavy chain
3	183.5	7.6	2116	2 A26655	myosin heavy chain
4	182	7.6	665	2 B71609	hypothetical prote
5	181	7.5	1790	2 S67593	transport protein
6	181	7.5	2464	1 QRMSPI	microtubule-associ
7	180	7.5	1871	2 D96796	probable heat choc
8	179.5	7.5	853	2 T51505	hypothetical prote
9	174.5	7.3	1526	2 A45605	mature-parasite-in
10	173	7.2	1558	2 B71603	RESA-H3 antigen pr
11	172.5	7.2	1979	2 C71622	hypothetical prote
12	171	7.1	2269	2 T28677	rhostry protein -
13	170.5	7.1	2364	2 A56577	microtubule-associ
14	169.5	7.1	1134	2 A60234	IgA FC receptor pr
15	169.5	7.1	1164	1 FCSOAG	IgA FC receptor pr
16	169.5	7.1	1392	2 A43336	microtubule-vesicl
17	169.5	7.1	1427	2 S22695	restin - human
18	169	7.0	1005	2 A64465	hypothetical prote
19	169	7.0	1909	2 A45592	liver stage antige
20	169	7.0	3488	2 T34418	hypothetical prote
21	168	7.0	1252	2 B42771	reticulocyte-bindi
22	168	7.0	1272	2 C90593	hypothetical prote
23	165.5	6.9	746	2 T47237	myosin II heavy ch
24	165.5	6.9	1804	2 T34518	nestin - golden ha
25	165	6.9	2401	2 T28676	rhostry protein -
26	164.5	6.8	5327	2 T13564	microtubule-associ
27	163.5	6.8	719	2 A81358	hypothetical prote
28	163.5	6.8	926	2 T24923	hypothetical prote
29	163.5	6.8	1169	2 T18423	hypothetical prote

30	163	6.8	976	2 T01553	hypothetical prote
31	162	6.7	1192	2 A71623	probable secreted
32	162	6.7	2663	1 S28261	centromere protein
33	161.5	6.7	1127	2 T28317	ORF MSV156 hypothe
34	161.5	6.7	1164	2 T24806	hypothetical prote
35	161.5	6.7	1577	2 T19722	hypothetical prote
36	161.5	6.7	1875	2 S38173	myosin-like protei
37	161.5	6.7	2385	2 A32491	myosin heavy chain
38	161.5	6.7	2411	2 B32491	myosin heavy body
39	161	6.7	944	2 S26710	spindle pole body
40	161	6.7	2510	2 T28160	hypothetical prote
41	160	6.7	1354	2 S74244	serine/threonine-s
42	159.5	6.6	1738	2 T14867	interactin - slime
43	159.5	6.6	2523	2 T18477	hypothetical prote
44	159	6.6	852	2 D72230	conserved hypothet
45	158.5	6.6	841	2 A86188	hypothetical prote

ALIGNMENTS

RESULT 1

A37180

chromogranin/secretogranin-like vesicle protein precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 30-Sep-1993

C:Accession: A37180

R:Ottinger, H.P.; Battenberg, E.F.; Tsou, A.P.; Bloom, F.E.; Sutcliffe, J.G.

J. Neurosci. 10, 3135-3147, 1990

A:Title: IB1075: a brain- and pituitary-specific mRNA that encodes a novel chromogran

A:Reference number: A37180; MUID:90376160; PMID:2204688

A:Accession: A37180

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-533 <OTT>

Query Match 80.8%; Score 1942; DB 2; Length 533;
Best Local Similarity 85.7%; Pred. No. 8e-89;
Matches 379; Conservative 23; Mismatches 40; Indels 0; Gaps 0;

QY	16	PIQAFPKGGSQDKSLHNREL	SAERPLNEQIAEAEADKIKKYP	PPENKPGQSNYSVDNL	75
DB	63	PNSFPKPGSQDKSLHNREL	SAERPLNEQIAEAEADKIKKYP	SEKSPERNFSSVDNL	122
QY	76	NLLRAITEKEKEKERQST	SRSSPLDNKLNVEDVDSTKNRKL	IDDYDSTKSGLDHFKQDDP	135
DB	123	NLLKAITEKETVEKAKQ	SRSPPFNRLNVDADSTKNRKL	IDYDSTKSGLDHFKQDDP	182
QY	136	DGLHOLDGTPLTAE	DIVHKIAARIYEENDRAVFDKIV	SKLLNLGLLITESQAHTLEDEVAE	195
DB	183	DGLHOLDGTPLTAE	DIVHKIATRIYEENDRGVFDKIV	SKLLNLGLLITESQAHTLEDEVAE	242
QY	196	VLOKLISKEANNYEED	PNKPTSWTENQAGKIEKVT	PMAAIODGLAKGENDET	255
DB	243	ALQKLISKEANNYEED	PNKPTSWTENQAGKIEKVT	PMVAATQDGTNRNDDT	302
QY	256	TNGLRRRTKTSYSE	DNFRDFOYFPNFVALLKSID	SEKAEKETLITIMKTLID	315
DB	303	SNGLERRNPHRDD	DFEELQYFPNFVALLTSID	SEKAEKETLITIMKTLID	362
QY	316	YGTISPEGVSYLEN	DEMIALQTKNLEKATNISK	LFPAPSEKSHETDSTKEAAK	375
DB	363	YGTISPEGVSYLEN	DEMIALQTKNLEKATNISK	LFPAPSEKSHETDSTKEAAK	422
QY	376	MEKEYGSLKDS	TKDSDNSPGGKTDEPKGT	EYALEAIRKNIEWLKHK	435
DB	423	MEKEYGSLKDS	TKDSDNSPGGKTDEPKGT	EYALEAIRKNIEWLKHK	482
QY	436	MRDFINKQADAY	VEKGILDKKEE	457	
DB	483	MRDFINQADAY	VEKGILIRKK	504	

Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: B71609
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-665 <GAR>
A:Cross-references: GB:AE001410; GB:AE001362; NID:g3845245; PIDN:AACT1925.1; PID:g384524
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: FFB0680w

Query Match 7.6%; Score 182; DB 2; Length 665;
Best Local Similarity 21.8%; Pred. No. 0.072;
Matches 103; Conservative 78; Mismatches 181; Indels 110; Gaps 17;
QY 25 GSQKSLNRLSARPLNEQIAEAEEDKIKKTYPPENKPGQSNYSFVDNLLRAITEK 84
DB 160 GKQDISNSNAE--NKKDVKEGVKELEKKKEEKISDDHKVKNKKS-----DD 205
QY 85 EKIEROSIRSSPLDNKLN---VEDVDSTKNRKLDDYDSTKSGLDHKKFODDPGLHQ 140
DB 206 HAVENKKSDDHKVEENKSSDDHKIEEVKKVEEHEDEEDKKEKSNKNKDNKDN 265
QY 141 LDGTPLTAEIDIVHKAARIYEENDRAVFDKIVSKLNLGLIPESQAHTLEDEVAEVLQKL 200
DB 266 EDNEISDEDEVDDEKNDIDDDK-----KETDKTHLEEEENELIEKE 314
QY 201 IS-KEANYEEDPNKPTGW-TENQAGKIPEKVTMPAAODGLAKGENDETSTNTLTNG 258
DB 315 FSDKKKNGKNDTKKSKDTEKSKDKIEK-----EKSKDKE----- 352
QY 259 LERRTKTYSEDNFRDQVFPNYPYALLKSDSEKAKEKETLITIMKTLIDFVKMVKYGT 318
DB 353 -KEKSKDEKEKKDKE-----KEKSKDIEKE-KDKDIEKSK-DTAKEKDKD 402
QY 319 ISPERGVSVLENLDEMIALQTKNLEKATDNISLFPAPSEKSH-----E 364
DB 403 IEKEKS-----KDMELKNQNDKDKDNEK-----KNDKQDIHDDNDNDMEETE 451
QY 365 ETDSTKEAAKME-----KEYSLKSDTK-DNSNPGGKTDEPKGTAYLRAI 412
DB 452 ENDEDEDEDENKKKKKKNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGNNGN 511
QY 413 KNIWELKKHDKGNKEDYDLSKMRDF-----INKQADAVVEKGILD 454
DB 512 NENENGEN 563

RESULT 5
S67593
transport protein USO1 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D252; protein YDLO58w
C:Species: Saccharomyces cerevisiae
C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 21-Jul-2000
C:Accession: S67593; A38455; S30782
R:Blöcker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67593
A:Molecule type: DNA
A:Residues: 1-1790 <BLQ>
A:Cross-references: EMBL:Z74106; NID:g1431058; PID:e253003; PID:g1431059; MIPS:YDLO58w
A:Experimental source: strain S288C
R:Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonehara, T.; Yoda, K.; Yamasaki, M.
J. Cell Biol. 113, 245-260, 1991
A:Title: A cytoskeleton-related gene, USO1, is required for intracellular protein transp
A:Reference number: A38455; MUID:91185402; PMID:2010462
A:Accession: A38455
A:Molecule type: DNA
A:Residues: 1-389, 'TA', 392-724, 'S', 726-1790 <NAK>
A:Cross-references: GB:X54378; NID:g4777; PIDN:CAA38253.1; PID:g4778
A>Note: the authors translated the codon ACT for residue 768 as Ile

R:Hostetter, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E
submitted to the EMBL Data Library, February 1993
A:Description: An integrin analogue in Saccharomyces cerevisiae.
A:Reference number: S30782
A:Accession: S30782
A:Molecule type: DNA
A:Residues: 71-846, 'E', 848-923, 'K', 925-1252, 'I', 1254-1318, 'V', 1320-1460, 'S', 1462-1580
A:Cross-references: EMBL:L03188
C:Genetics:
A:Gene: SGD:USO1; INT1
A:Cross-references: SGD:S0002216; MIPS:YDLO58w
A:Map position: 4L
C:Keywords: coiled; transmembrane protein
F:326-342/Domain: transmembrane #status predicted <TM1>
F:394-410/Domain: transmembrane #status predicted <TM2>
F:617-633/Domain: transmembrane #status predicted <TM3>

Query Match 7.5%; Score 181; DB 2; Length 1790;
Best Local Similarity 19.9%; Pred. No. 0.28;
Matches 118; Conservative 102; Mismatches 176; Indels 196; Gaps 28;
QY 30 SLHNRELSARPLNEQIAEA--EEDKIKKTYPPENKPGQSNYSFVDNLLRAITEKEKI 87
DB 748 SLQTESPHENLTKELIALTNEHKELDEKYQILN--SSHSLKENFSIL----- 795
QY 88 EXEROSIRSSPLDNKLNVEDVDSTK---NRKLDDYDSTKSGLDHKKFOD---PDGLHQ 140
DB 796 ETELKNRDS-IDEMTQLDKRVLETCKENGTALLEYKST-----IHQAQESIKTLEKLET 850
QY 141 LDGTPLTAEIDIVHKAARIY-----EEN-----DRAVFDKIVS 173
DB 851 ILSQKKAEEDGINKMGKDLFALSREMQAEECNKLNQKBDKSNVNHQKETSLEKEDIAA 910
QY 174 KLLNLGLIPES-----QAHTLEDEVAEVLQKLISKEANNYEDPNKPTSWTENQAKIP 227
DB 911 KITEIKAINLENLEEMKIQCNLSKEKEHISKELVEYKSRFQSHD-----NLVAKLT 961
QY 228 EKVTPMA-----AIDQGLAKGENDETSTNTLTNGLERRTKTYSEDNFRDQ---- 275
DB 962 EKLKSLANNYKDMAENSLIKAVESKNESLIQSN-LQNKIDSNSQEK-ENFQTERGS 1019
QY 276 YFPNYPYALKSIDSEKAKEK-----ETLITIMKTLIDFVKMVKYGTISPESGVSYL-- 328
DB 1020 IEKNIEQLKKTISDLQTEQTEIISKSDSKDEYESIQLLKEKLETATTANDENVNKISE 1079
QY 329 -----ENLDEMTA-----LOTNKK-----LEKNATD---- 349
DB 1080 LTKTREELAEALAAAYKNLKNLETKLETSEKALKEYKNEHLEKKEIKQLEKEATETKQ 1139
QY 350 -----NISKLPAPSEKSHETDST---KEAAKMEKEY---GSLKD---STKDDNS 392
DB 1140 LNSLRANLESL-----EKEHEDLAAQLKKYEQIANKQYNEEISQLNDEITSTQGENE 1194
QY 393 NPGGKTDEPKGTAEY-----LEAIRKNIDMLKKHKKKG----- 426
DB 1195 SIKKKNDELEGEVAKMKSSTSEOSNLKKSEIDALNLQIKELKKNETNEASLESIKSVE 1254
QY 427 -----NKEDYDLSKMRDPIKQAD---AYVEKGILDKEEAFAIK 462
DB 1255 SETVTKIKELQDECNFKEKVESELEDKASKEDKNKSYLEL-----QKSEKIK 1302

RESULT 6
QRMSPI
microtubule-associated protein MAP1B - mouse
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated pro
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 01-Sep-2000
C:Accession: S07545; S44387; A33645
R:Noble, M.; Lewis, S.A.; Cowan, N.J.
J. Cell Biol. 109, 3367-3376, 1989
A:Title: The microtubule binding domain of microtubule-associated protein MAP1B conta
A:Reference number: A33645; MUID:90094539; PMID:2480963


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Qy      80 A-----ITEKEK--IEKERQSIRSSPLDNKLNVEDVDSTKNRKLID-----DYDSTKSGLDH 129
Db      202 EKELDINKREKKINEKKNIIKKEETFHFHNIEKEYLEKKNKERETISIEIITDIKKHLKELKI 261
Qy     130 KFQDDPGLHOLDPTLTAEDIVHKIAARIYEEND--RAVFDKIYSKLLNLGLITESOAH 187
Db     262 EIKKKEDLENLKLSKENVLKELGCVKEKNETINSLNDNIIEK-----EKKYK 313
Qy     188 TLEDEVAEVLQK--LISKEANNYBEDPNKPTSWTENQAGKIPEKVTPMAAIODGLAKGEN 245
Db     314 LLEYELEKKNQOIDLLNKQEKEKEKEKEKE---KEKEKEKEKE-----YDTLIKELK 364
Qy     246 DETYS-----NTLTTLNGLERRTKTY--SEDNFRDFQ--YPPN-----FYALLKSIDS 289
Db     365 DEKISILEKVHSIKVREMEDIKREHNFUHMEDQLDKNSFVKNNNQLVKAYKCEIKNKT 424
Qy     290 EKEAKE-----KETLTIIMKTLTDFVVMVMYGYTISPESBEGSVSYLENIDEMIALOT 339
Db     425 ELEKKEKELKDIENTVSKEEINKLNQNLKEKEQILAFNKNHKEETHGLKEELKESYKI-- 482
Qy     340 KNKLE----KNATDNISKLPAPSEKSHHEETDSTKEEAAMBEKYGSLKSDTSKDDNSNP 395
Db     483 -TKIETOELQEMVDIKOELDOLQBKYNAQIESISIELSKKEKEYNQYKNTYIEELNUN 541
Qy     396 KGTDEP-----RGKTEAYLEAIRKNTEWLKHKDKGNKEDYDLKMRDFINKQADAY- 447
Db     542 EKLEETNKETYNLQNNYTNEINMLNNDIHMLNGNIKTNWQTISTLKNDVHLLNEQIDKLN 601
Qy     448 VEKGILDKEEAF 459
Db     602 NEKGTLSNKISE 613

RESULT 12
T28677
rhoptry protein - Plasmodium yoelii
C:Species: Plasmodium yoelii
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C:Accession: T28677; C45521
R:Keen, J.; Sinha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
A>Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium
A:Reference number: Z20508; MUID:95021522; PMID:7935623
A:Accession: T28677
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2269 <KE>
R:Cross-references: EMBL:L27838; NID:g457145; PID:g457146; PIDN:AAA21304.1
A:Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A>Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. M.
A:Reference number: A45521; MUID:91101660; PMID:2270106
A:Accession: C45521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 2131-2269 <KE2>
A:Cross-references: GB:M34283

Query Match          7.1%; Score 171; DB 2; Length 2269;
Best Local Similarity 20.9%; Pred. No. 1.2;
Matches 112; Conservative 83; Mismatches 196; Indels 144; Gaps

Qy    13 LVLPQIAFPFGGSQDSKLNRSLRSALRPLNEQIAAEEDIKKTYPPENPGOSNYSV 72
Db    7 LIPLPMNQFGLNESMIKLNKSGILRKYYTINSQI-----KNKLNVSYPEGREG-----FT 57
Qy   73 DNLNL-----LRATEKEK-----IEKRQSIRSSPLDN-----KLN- 104
Db   58 SSLELAWSWEKTKLETITELTSNEETVRLEKEIRELFPKYLDEAERKYLEGLEKLELNK 117
Qy  105 -----VEDVNST-----KNRKLID-----DYDSTKSGLDH 129
Db  118 KIKDITAKIEVKNTVKELKEIKNNAYIDELANOSPKYVTGYTENKNTYINTIKSYFDO 177

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Qy 308 DFKVMVAVYGTISPEEGVSVYLENDIMIALQTNKL---EKNATDNLISKL-----FPAP 358
Db 783 -----KGSAPSEDEGITTTGEGE--CQQTPEEPVKVQGVDDTEKFEDEGAGFEES 833
Qy 359 SEKSHEETDTKTEAAKMEKEYSLKDKSTDDNSNPGKTDPEKPKTEA--YLEIAIRKNI 416
Db 834 SEAGDYEEKAETEAEEAPEEDG---EDNVSGSASKHSPTDEETAKAEADVHIKKEKESV 890
Qy 417 -----EWLKHKDKKGNKEDYDLKSKMRDFINKQADAVYVEKGIILKEAE 459
Db 891 ASGDRAEDAEQDALEKGEAQSEEGEEEEE-----DKAEDAREEDHEPDKTEAE 940

RESULT 14
A60234
Iga Fc receptor precursor - Streptococcus agalactiae (strain SB35)
N:Alternate names: Iga-binding protein; protein Bac
N:Contains: beta antigen
C:Species: Streptococcus agalactiae
C:Date: 08-Dec-1992 #sequence.revision 08-Dec-1992 #text_change 26-Aug-1999
C:Accession: A60234; S14595; A60230
R:Heden, L.O.; Frithz, E.; Lindahl, G.
Eur. J. Immunol. 21, 1481-1490, 1991
A:Title: Molecular characterization of an Iga receptor from group B streptococci
  with Iga-binding capacity.
A:Reference number: A60234; MUID:91257158; PMID:2044657
A:Accession: A60234
A:Molecule type: DNA
A:Residues: 1-1134 <HED>
A:Cross-references: EMBL:X58470; NID:946520; PIDN:CAA41384.1; PID:946521
A:Note: the source is designated as group B streptococcus strain SB35
R:Heden, L.; Frithz, E.; Lindahl, G.
Submitted to the EMBL Data Library, March 1991

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A:Description: Molecular characterization of an IgA receptor from group B streptococcus fragments.
A:Reference number: S14595
A:Accession: S14595
A:Molecule type: DNA
A:Residues: 1-1134 <HE2>
A:Cross-references: EMBL:X58470; NID:g46520; PIDN:CAA1384.1; PID:g46521
A:Note: the source is designated as Streptococcus agalactiae
R:Lindahl, G.; Akerstrom, B.; Vaermat, J.P.; Stenberg, L.
Eur. J. Immunol. 20, 2241-2247, 1990
A:Title: Characterization of an IgA receptor from group B streptococci: specific

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A:Reference number: A60230; MOLD:91055597; PMID:2242758
A:Accession: A60230
A:Molecule type: protein
A:Residues: 'X',39-48,'X',54-56 <LIN>
C:Superfamily: Iga Fc receptor
C:Keywords: cell wall; immunoglobulin receptor; tandem repeat; transmembrane pr
F:1-37/Domain: signal sequence #status predicted <SIG>
F:38-1134/Product: Iga Fc receptor #status experimental <MAT>
F:199-438/Domain: Iga binding #status predicted <IGAL>
F:439-826/Domain: Iga binding #status predicted <IGA2>
F:827-915/Region: proline-rich repeats
F:916-1101/Domain: cell wall-spanning #status predicted <CWS>
F:1102-1129/Domain: transmembrane #status predicted <TMW>

Query Match          7.1%  Score 169.5;  DB 2;  Length 1134;
Best Local Similarity 21.4%;  Pred. No. 0.58;
Matches 123;  Conservative 78;  Mismatches 189;  Indels 185;  Gaps 25;

Qy      36  LSAERPLNE-----QIAEAEEDTKTKYPPENKPGQSNYSFVDNLLRAIT-BKEK  86
Db      149  LELENQNETNRLHLIKHOEEVEKDKRAK---QQKTLKQSDTKVLSNDKELNHHQSK  204
Qy      87  IEK--EQGSTRSSPLDNKL-----NVEDVDSTKNRKLLDDYDSTKSGLDHK  130
Db      205  VERMAEQKGITNEDKDSMLKIEDIRKQAQAQAKKDEAEVKEELCKLFSSYTKAGLDQE  264
Qy      131  FQDDPDGLHLDGTPLTAEDIVHKI-----AARTYEENDRAVFDKIYKSLNLNG  179

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Qy	87	IEK---EQRSIRSSPLDNKL-----NVEDVDSTKRNKRLIDDYDSTKSGLDHK	130
Db	205	VEKMAEQKGTINDEKDSMLKIEDIRKQAQADKKDEAEVREVLGKLFSTKAGLQDE	264
Qy	131	FQDDPDGLHOLDGTPLTAEDIVHKI-----AARIYEENDRAVEDKIVSKLLNLG	179
Db	265	IQE-----HVKKET--SSEENTQKVDEHYANSQNLQAQKSLLEELD KATTNQAQTVQKNQF	317
Qy	180	L-----ITESAHTLEDEVAEV-----LOKLSKE---ANNYEE	210
Db	318	LENAQKLKEIQPLIKETNVKLYKAMSELSQVEKELKHNSLEANLEDLVAKSKETVREYG	377
Qy	211	DPNKTSWTE-----NOAGKIPEKVTPEMAAIOGLAKGENDETSVN	251
Db	378	KLNQSKNLPQLQLEEAHSHKLQOVVEDFRKKFTSEQVTPKKRVKRDLANENNQ---	434
Qy	252	TLTLNGLNRLRTKTVSYSDNFRDQYFPNFYALLKSIDSEKAKEKETLITIMKTLIDFVK	311
Db	435	KIELTVSPENITVVEGED-----VKFTVTAKS-DS-----KTTLDFSD	471
Qy	312	MMVKYG-TISPEEGSVYLENLD-----EMIALQTK-----NKLEKNATD	349
Db	472	LLTKYNPVSVDRLSTNKTNTDHHKIAETIKNLKLNESQTVTLKADDDSGNVVEKFTTI	531
Qy	350	NISKLPAPSEKSHETDSTYKEBA-----KMEKEYGSLKD	385
Db	532	TVQKKEEKQVPKTPQEKDSKTEEKVPOEPKSDKNQLQELITKSAQOELEKAIKELME	591
Qy	386	STKDDNSPGGKDEPKGKTEAYLEATRKNIEMLKK---HDKGNKEDYLSKMRQFIN	441
Db	592	Q-PEIFSNP--EYGIQKSIWESOKEPTQEAITFSKKILIGDSSSKYYTEHYFNKYKSDFMN	648
Qy	442	KQADAYVEGILDKPEAE-----AIKRIYSS	467
Db	649	YQLHAQME--MLTRKVVQVMNKYPDNAEIKKIFES	681

R:Jerlstroem, P.G.; Chhatwal, G.S.; Timmis, K.N.
Mol. Microbiol. 5, 843-849, 1991
A:Title: The IgA-binding beta antigen of the c protein complex of Group B streptococci.
A:Reference number: S15330; MUID:91312121; PMID:1857207

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Query Match      7.1%  Score 169.5;  DB 1;  Length 1164;
Best Local Similarity 21.4%;  Pred. No. 0.6;
Matches 123;  Conservative 78;  Mismatches 189;  Indels 185;  Gaps 25;

QY 36 LSAERPLNE-----QIAEAEEDRIKITYPPENKPGOSYFVGNLNLRAIT-EKEK 86
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
149 LELEQNFETNRLHLIKOHEEVEKDKKAR-----QQETLKQSDPTKVDLSNIDKELNHQKS 204

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 08:26:12 ; Search time 36 seconds
(without alignments)
611.347 Million cell updates/sec

Title: US-09-554-945b-2

Perfect score: 2402

Sequence: 1 MGFLGTGTLVLLVLPQIAF.....EKGILDKPEAEAKRIYSSL 468

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2380	99.1	468	1 SG3_HUMAN	Q8wxd2 homo sapien
2	2093.5	87.2	471	1 SG3_MOUSE	P47867 mus musculus
3	2081.5	86.7	471	1 SG3_RAT	P47868 rattus norv
4	183.5	7.6	2116	1 MYS2_DICDI	P08799 dictyosteli
5	181	7.5	882	1 RAS0_PYFU	P58301 pyrococcus
6	181	7.5	1790	1 US01_YEAST	P25386 saccharomyc
7	181	7.5	2454	1 MABP_MOUSE	P14873 mus musculus
8	170.5	7.1	2459	1 MABP_RAT	P15205 rattus norv
9	169.5	7.1	1164	1 BAG_STRAG	P27951 streptococc
10	169.5	7.1	1427	1 REST_HUMAN	P30622 homo sapien
11	169	7.0	1005	1 RAS0_METJA	Q58718 methanococc
12	168	7.0	1251	1 RBP2_PLAVB	Q00799 plasmodium
13	166	6.9	700	1 TRDN_CANFA	P82179 canis famill
14	162.5	6.8	957	1 KFSC_HUMAN	O60282 homo sapien
15	162	6.7	2863	1 CENE_HUMAN	Q02224 homo sapien
16	162	6.7	5038	1 PCLO_MOUSE	Q09yx7 mus musculus
17	161.5	6.7	1875	1 MLP1_YEAST	Q02455 saccharomyc
18	161	6.7	944	1 NUF1_YEAST	P23280 saccharomyc
19	159.5	6.6	2230	1 GOG4_HUMAN	Q13439 homo sapien
20	159	6.6	852	1 RAS0_THEMA	Q9X1x1 thermotoga
21	158.5	6.6	956	1 KFSC_MOUSE	P28738 mus musculus
22	157.5	6.6	1978	1 MYHB_CHICK	P10587 gallus gall
23	157	6.5	2022	1 ANP1_ONCVO	P21249 onchocerca
24	156.5	6.5	1969	1 MYS2_CAEEL	P12844 caenorhabdi
25	156.5	6.5	1972	1 MYHB_HUMAN	P35749 homo sapien
26	156	6.5	839	1 COB2_YEAST	P53959 saccharomyc
27	156	6.5	1208	1 PCPL_SCHPO	Q92351 schizosacch
28	155.5	6.5	1526	1 MYS1_SCHPO	Q9us16 schizosacch
29	155	6.5	705	1 TRDN_RABIT	Q28820 oryctolagus
30	154.5	6.4	997	1 SCPL_RAT	Q03410 rattus norv
31	154	6.4	727	1 MFPI_ARATH	Q91w85 arabidopsis
32	153.5	6.4	1130	1 YL17_CAEEL	Q11102 caenorhabdi
33	153.5	6.4	2104	1 MYS3_SCHPO	Q14157 schizosacch

34	153	6.4	1433	1 REST_CHICK	O42184 gallus gall
35	152.5	6.3	1972	1 MYHB_RABIT	P35748 oryctolagus
36	152	6.3	1957	1 SPOF_SCHPO	Q10411 schizosacch
37	152	6.3	1962	1 MYS2_DROME	P05661 drosophila
38	151.5	6.3	1044	1 YAF3_SCHPO	Q09857 schizosacch
39	151.5	6.3	1360	1 CING_XENLA	Q9pdc7 xenopus lae
40	151.5	6.3	5085	1 PCLO_RAT	Q9jks6 rattus norv
41	150.5	6.3	1539	1 Y373_HUMAN	O15078 homo sapien
42	150.5	6.3	1630	1 MSPL_PLAFK	P04932 plasmodium
43	150.5	6.3	1639	1 MSPL_PLAFW	P04933 plasmodium
44	150.5	6.3	1976	1 MYHA_RAT	Q9jlt0 rattus norv
45	149	6.2	991	1 SCA4_RICAU	Q9aj64 rickettsia

ALIGNMENTS

RESULT 1
SG3_HUMAN
ID SG3_HUMAN STANDARD; PRT; 468 AA.
AC Q8WXD2; Q96G83; Q96G88; Q9Y6G7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Secretogranin III precursor (SgIII).
GN SGC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RA Song H., Peng Y., Huang Q., Dai M., Mao Y., Zhang Q., Mao M., Fu G.,
RA Luo M., Chen J., Hu R.;
RT "Human secretogranin III mRNA, complete cds.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX MEDLINE=22093564; PubMed=12098761;
RA Rong Y.P., Liu F., Zeng L.C., Ma W.J., Wei D.Z., Han Z.G.;
RT "Cloning and characterization of a novel human secretory protein: secretogranin III.";
RL Acta Biochim. Biophys. Sin. 34:411-417(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Trimmwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted. Neuroendocrine and endocrine secretory granules.
CC -!- TISSUE SPECIFICITY: Expressed in brain, heart, kidney, liver and skeletal muscle.

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EMBL; AF078851; AAD44483.1; -
 EMBL; AF453583; AAL67431.1; -
 EMBL; BC014539; AAH14539.1; -
 EMBL; BC009511; AAH09511.1; ALT_INIT.
 Genew; HGNC:13707; SCG3.
 KW Signal; Cleavage on pair of basic residues; Polymorphism.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 468 SECRETORANIN III.
 FT VARIANT 125 125 S -> N (in dSNP:2305710).
 FT CONFLICT 79 79 K -> R (IN REF. 1).
 FT CONFLICT 167 167 A -> V (IN REF. 1 AND 2).
 FT CONFLICT 272 274 EEL -> RDF (IN REF. 1).
 SQ SEQUENCE 468 AA; 52977 MW; 633A87692A783808 CRC64;

Query Match 99.1%; Score 2380; DB 1; Length 468;
 Best Local Similarity 98.9%; Pred. No. 1.7e-107;
 Matches 463; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPRLNQLQIAEAEEDKTKKTPP 60
 DB 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPRLNQLQIAEAEEDKTKKTPP 60
 QY 61 ENKPGQSNYSFVDNLLRLRAITEKEKEKESQSRSSPLDNKLNVEDVDSTKKNKLDDY 120
 DB 61 ENKPGQSNYSFVDNLLRLRAITEKEKEKESQSRSSPLDNKLNVEDVDSTKKNKLDDY 120
 QY 121 DSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKTVSKLLNGL 180
 DB 121 DSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKTVSKLLNGL 180
 QY 181 ITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPMAIODGL 240
 DB 181 ITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPMAIODGL 240
 QY 241 AKGNETVSNLTTLTNGLERRTKYSSEDFRQYFPNFPYALLKSIDSEKAKEKTLI 300
 DB 241 AKGNETVSNLTTLTNGLERRTKYSSEDFRQYFPNFPYALLKSIDSEKAKEKTLI 300
 QY 301 TIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLPAPSE 360
 DB 301 TIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLPAPSE 360
 QY 361 KSHEETDSTKEAAKMEKEYSGLKSDSTKDDNSNPGGKTDPKGTAYLEAIRKNIEWLK 420
 DB 361 KSHEETDSTKEAAKMEKEYSGLKSDSTKDDNSNPGGKTDPKGTAYLEAIRKNIEWLK 420
 QY 421 KHKKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAKRIYSSSL 468
 DB 421 KHKKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAKRIYSSSL 468

RESULT 2
 SG3_MOUSE
 ID SG3_MOUSE STANDARD; PRT; 471 AA.
 AC P47867;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secretorin III precursor (SgIII).
 GN SCG3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=95001263; PubMed=7917832;
 RA Dopazo A., Lovenberg T.W., Danielson P.E., Ottiger H.-P.,
 RA Sutcliffe J.G.;
 RT "Primary structure of mouse secretorin III and its absence from
 deficient mice";
 RL J. Mol. Neurosci. 4:225-233(1993).
 CC -!- SUBCELLULAR LOCATION: Secreted. Neuroendocrine and endocrine
 CC secretory granules.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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EMBL; U02982; AAA56636.1; -
 MGD; MGI:103032; Scg3.
 KW Signal; Cleavage on pair of basic residues.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 471 SECRETORANIN III.
 SQ SEQUENCE 471 AA; 53326 MW; FC1E9C381AFCA564 CRC64;

Query Match 87.2%; Score 2093.5; DB 1; Length 471;
 Best Local Similarity 87.9%; Pred. No. 9.1e-94;
 Matches 414; Conservative 17; Mismatches 37; Indels 3; Gaps 1;

QY 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPRLNQLQIAEAEEDKTKKTPP 57
 DB 1 MGFLGTGFWILVLPQAPKPGSQDSKLSHRELSEALPRLNQLQIAEAEEDKTKKTPP 60
 QY 58 YPENKPGQSNYSFVDNLLRLRAITEKEKEKESQSRSSPLDNKLNVEDVDSTKKNKLI 117
 DB 61 FPSEKSPSESNYSVDNLLRLRAITEKEKEKESQSRSSPLDNKLNVEDVDSTKKNKLI 120
 QY 118 DQDSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKTVSKLLN 177
 DB 121 DEYDSTKSGLDHFKQDDPGLHQLDGTPLTAEDIVHKAIRIYEENDRAVFDKTVSKLLN 180
 QY 178 LGLITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPMAI 237
 DB 181 LGLITESQAHTLEDEVAEVLQKLISKANNYEEDPNKPTSWTENQAGKIPEKVTMPMAI 240
 QY 238 DGLAKGNETVSNLTTLTNGLERRTKYSSEDFRQYFPNFPYALLKSIDSEKAKEKE 297
 DB 241 DGFTNREDETSTKEAAKMEKEYSGLKSDSTKDDNSNPGGKTDPKGTAYLEAIRKNIE 300
 QY 298 TLITIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLP 357
 DB 301 TLITIMKTLIDFVKMVKYGTISPESGVSYLENDEMIALQTKNLEKNATDNISKLP 360
 QY 358 PSKSHHEETDSTKEAAKMEKEYSGLKSDSTKDDNSNPGGKTDPKGTAYLEAIRKNIE 417
 DB 361 PPESKSHHEETDSTKEAAKMEKEYSGLKSDSTKDDNSNPGGKTDPKGTAYLEAIRKNIE 420
 QY 418 WLKHKKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAKRIYSSSL 468
 DB 421 WLKHKKGKEDYDLSKMRDFINQADAYVEKGIIDKEAEAKRIYSSSL 471

RESULT 3
 SG3_RAT
 ID SG3_RAT STANDARD; PRT; 471 AA.
 AC P47868;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Secretorin III precursor (SgIII) (181075).
 GN SCG3.

```
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95001263; PubMed=7917832;
RA Dopazo A., Lovenberg T.W., Danielson P.E., Ottiger H.-P.,
RA Sutcliffe J.G.;
RT "Primary structure of mouse secretogranin III and its absence from
RT deficient mice.";
RL J. Mol. Neurosci. 4:225-233(1993).
RN [2]
RP PRELIMINARY SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90376160; PubMed=2204688;
RA Ottiger H.-P., Battenberg E.F., Tsou A.-P., Bloom F.E.,
RA Sutcliffe J.G.;
RT "1B1075: a brain- and pituitary-specific mRNA that encodes a novel
RT chromogranin / Secretogranin-like component of intracellular
RT vesicles.";
RL J. Neurosci. 10:3135-3147(1990).
CC -!- SUBCELLULAR LOCATION: Secreted. Neuroendocrine and endocrine
CC secretory granules.
CC -!- TISSUE SPECIFICITY: BRAIN- AND PITUITARY-SPECIFIC.
CC -----
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CC -----
DR EMBL: U02983; AAA56637.1; -.
KW Signal; Cleavage on pair of basic residues.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 471 SECRETOGRANIN III.
SQ SEQUENCE 471 AA; 53183 MW; 977B3F885F33223 CRC64;
Query Match 86.7%; Score 2081.5; DB 1; Length 471;
Best Local Similarity 87.0%; Pred. No. 3.4e-93;
Matches 410; Conservative 20; Mismatches 38; Indels 3; Gaps 1;
QY 1 MGFLGTGWILVLV---PIQAFKPGSQDKSLHNRELSAERPLNEQIAEAEDKIKKT 57
DB 1 MGFLWTGSMILVLVNSGPIQAFKPGSQDKSLHNRELSAERPLNEQIAEAEDKIKKT 60
QY 58 YPPENKPCQSNVFDVNLNLRATEKEKIKEROSIRSSPLDNKLVNVEDVDSTKNKLI 117
DB 61 YPSEKPSSESFSSVDNLLKKAITEKETVEKAKOSIRSSPFDNRLNVDDADSTKNRKL 120
QY 118 DDYDSTKSLGDKHKKFDDPDGLHLDGTLPTAEDIVHKTAARIYEENDRAVDFKIVSKLLN 177
DB 121 DEYDSTKSLGDKHKKVDDPDGLHLDGTLPTAEDIVHKTAARIYEENDRGVDFKIVSKLLN 180
QY 178 LGLITESQAHTLEDEVAELVLOKLSKEANNYEEDPNKPTSWTENQAGRIPEKVTPTMAAIQ 237
DB 181 LGLITESQAHTLEDEVAELVLOKLSKEANNYEAEPEKTSRTENQDGRIPEKVTPTAATQ 240
QY 238 DGLAGKENDETVSNPLTNTGLERTKTYTSEDNFRDQYFPNFPYALLKSIDSEKAKEKE 297
DB 241 DGTFTNREDDTVSNPLTNSGLERTNPHRDDDFEELQYFPNFPYALLTSIDSEKAKEKE 300
QY 298 TLITITMKTLIDFVKMWVYKGISPEEGYSYLENDEMIALQTKNKLKNATDNISKLPFA 357
DB 301 TLITITMKTLIDFVKMWVYKGISPEEGYSYLENDEMIALQTKNKLKNATDNISKLPFA 360
QY 358 PSEKSHETDSTKEAAKWEKYGSLKDKDSDNSPGSKTDEPKGTEAYLEATRKNTIE 417
DB 361 PPKSHETDSTKEAAKWEKYGSLKDKDSDNSPGSKTDEPKGTEAYLEATRKNTIE 420
QY 418 WLKHKHDKGNKEDYDLSKMRDQFINQADAYVEKIGILDKEEAIAIKRIYSSL 468
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DB 421 WLKHKHDKGNKEDYDLSKMRDQFINQADAYVEKIGILDKEEAIAIKRIYSSL 471
RESULT 4
MYS2_DICDI STANDARD; PRT; 2116 AA.
AC P08799;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Myosin II heavy chain, non muscle.
GN MHCA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87092266; PubMed=3540939;
RA Warrick H.M., de Lozanne A., Levinwand L.A., Spudich J.A.;
RT "Conserved protein domains in a myosin heavy chain gene from
RT Dictyostelium discoideum.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9433-9437(1986).
RN [2]
RP PHOSPHORYLATION SITES, AND MUTAGENESIS.
RC STRAIN=AX2;
RX MEDLINE=90353583; PubMed=2387408;
RA Lueck-Vielmeier D., Schleicher M., Grabatin B., Wippler J.,
RA Gerisch G.;
RT "Replacement of threonine residues by serine and alanine in a
RT phosphorylatable heavy chain fragment of Dictyostelium myosin II.";
RL FEBS Lett. 269:239-243(1990).
RN [3]
RP PHOSPHORYLATION SITES.
RX MEDLINE=88112226; PubMed=2828113;
RA Wagle G., Noegel A., Scheel J., Gerisch G.;
RT "Phosphorylation of threonine residues on cloned fragments of the
RT Dictyostelium myosin heavy chain.";
RL FEBS Lett. 227:71-75(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.
RX MEDLINE=95345066; PubMed=7619795;
RA Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M.,
RA Rayment I.;
RT "X-ray structures of the myosin motor domain of Dictyostelium
RT discoideum complexed with MgADP.Befx and MgADP.ALf4-.";
RL Biochemistry 34:8960-8972(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 1-762.
RX MEDLINE=95345067; PubMed=7619796;
RA Smith C.A., Rayment I.;
RT "X-ray structure of the magnesium(II)-pyrophosphate complex of the
RT truncated head of Dictyostelium discoideum myosin to 2.7-A
RT resolution.";
RL Biochemistry 34:8973-8981(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
RX MEDLINE=96206189; PubMed=8611530;
RA Smith C.A., Rayment I.;
RT "X-ray structure of the magnesium(II).ADP.vanadate complex of the
RT Dictyostelium discoideum myosin motor domain to 1.9-A resolution.";
RL Biochemistry 35:5404-5417(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.
RX MEDLINE=97452580; PubMed=9305951;
RA Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
RT "X-ray structures of the MgADP, MgATPgammAS, and MgAMPNP complexes
RT of the Dictyostelium discoideum myosin motor domain.";
RL Biochemistry 36:11619-11628(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
RX MEDLINE=98070605; PubMed=9405148;
RA Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
```

"X-ray crystal structure and solution fluorescence characterization of Mg₂.(3')-O-(N-methylanthraniloyl) nucleotides bound to the Dictyostelium discoidium myosin motor domain.";
 J. Mol. Biol. 274:394-407(1997).
 -1- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN.
 -1- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 -1- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL CORTEX.
 -1- DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN BE FURTHER SPLIT INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).
 -1- DOMAIN: THE ROD-LIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 -1- PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION AND REDUCES THE ACTIN-ACTIVATED ATPASE ACTIVITY.
 -1- MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA ATPASE ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS AT THE SH-1 POSITION (688).
 -1- SIMILARITY: Contains 1 myosin-like globular head domain.
 -1- SIMILARITY: Contains 1 IQ domain.

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 EMBL; M14628; AAA3227.1; .
 PIR; A26655; A26655.
 PDB; 1MMA; 03-DEC-97.
 PDB; 1MMD; 17-AUG-96.
 PDB; 1MMG; 03-DEC-97.
 PDB; 1MMN; 03-DEC-97.
 PDB; 1MND; 17-AUG-96.
 PDB; 1MNE; 17-AUG-96.
 PDB; 1VON; 23-DEC-96.
 PDB; 1LXK; 28-JAN-98.
 PDB; 1DOX; 20-DEC-00.
 PDB; 1DOY; 20-DEC-00.
 PDB; 1DOZ; 20-DEC-00.
 PDB; 1DIA; 20-DEC-00.
 PDB; 1DIB; 20-DEC-00.
 PDB; 1FMV; 20-DEC-00.
 PDB; 1FMW; 20-DEC-00.
 PDB; 1G8X; 17-JAN-01.
 PDB; 1JWI; 07-NOV-01.
 PDB; 1JX2; 07-NOV-01.
 DictyDb; DD01008; mhca.
 InterPro; IPR000048; IQ-region.
 InterPro; IPR001609; myosin_head.
 InterPro; IPR004009; Myosin_N.
 Pfam; PF00612; IQ; 2.
 Pfam; PF00663; myosin_head; 1.
 Pfam; PF02736; Myosin_N; 1.
 PRINTS; PR00193; MYOSINHEAVY.
 ProDom; PD000355; myosin_head; 1.
 SMART; SM00015; IQ; 1.
 SMART; SM00242; MYSC; 1.
 SMART; PS50096; IQ; 1.
 Myosin; Coiled coil; Actin-binding; ATP-binding; 3D-structure;
 Calmodulin-binding; Methylation; Alkylation; phosphorylation.
 DOMAIN 1 761
 FT DOMAIN 762
 FT DOMAIN 817 2116
 FT COILED COIL (POTENTIAL).

FT NP_BIND	179	186
FT DOMAIN	638	660
FT DOMAIN	738	752
FT MOD_RES	130	130
FT MOD_RES	678	678
FT MOD_RES	1823	1823
FT MOD_RES	1833	1833
FT MOD_RES	2029	2029
FT TURN	3	5
FT TURN	7	8
FT HELIX	10	15
FT HELIX	25	28
FT STRAND	34	37
FT TURN	41	42
FT STRAND	48	55
FT STRAND	59	63
FT STRAND	69	73
FT HELIX	74	76
FT STRAND	78	79
FT HELIX	83	85
FT TURN	86	87
FT STRAND	90	90
FT HELIX	91	93
FT TURN	99	110
FT TURN	111	113
FT STRAND	116	119
FT TURN	120	121
FT STRAND	122	126
FT HELIX	137	142
FT TURN	143	145
FT HELIX	148	150
FT HELIX	155	169
FT TURN	170	170
FT STRAND	173	179
FT TURN	181	182
FT HELIX	185	200
FT HELIX	210	226
FT STRAND	227	228
FT TURN	234	235
FT STRAND	236	237
FT STRAND	240	247
FT TURN	249	250
FT STRAND	253	261
FT HELIX	265	268
FT TURN	269	269
FT TURN	273	274
FT STRAND	278	278
FT HELIX	279	287
FT TURN	290	296
FT TURN	297	297
FT TURN	301	303
FT TURN	305	307
FT TURN	316	317
FT HELIX	320	334
FT TURN	335	335
FT HELIX	338	355
FT TURN	356	356
FT STRAND	360	360
FT STRAND	368	368
FT HELIX	373	382

Query Match 7.6%; Score 183.5; DB 1; Length 2116;

Best Local Similarity 21.6%; Pred. No. 0.18;

Matches 108; Conservative 86; Mismatches 205; Indels 101; Gaps 17;

QY 26 SQDKS--LHNRELSAERPLNEQTAEEDEKIKKTYPPENKPGQSNYSFVDNLNLLRAITE 83

Db 1023 TKDKSELLRQKKLEELKQVQEAALAAETAAKLAQEAANKLQGEVTEL-NEKFNSEVTA 1081

QY 84 KEKIEKERSIRSS--PLDNKLNVEDVDSTKRNKLIIDDYDSTKSGLDHKFQDDPDGLHQL 141

Db 1082 RSNVEKSKTLESQVAVNNDEE-----KKNR---DALEKKKKALDAMLEEMKQDLEST 1134

QY 142 DGTPLTAEDIVHIAIRIYEENDRAVDKIVSKLLNLGLITESQAHTLEDEVAEVLQKLI 201
Db 1135 GEEKKSLYDL-----KVKQSDMEALRNQISLOSTIAKLEKIKSTLEGEVARLOGELE 1188
QY 202 SKE--ANNYEEDPNKPTSWENOGAKIPEKVT-----PMAIODGLAKGEN 245
Db 1189 AEOLAKSNVEKQKKVLELDEKDSQAIAETAAKQALDKLKKLEQELSEVQTLSEANN 1248
QY 246 D-----ETVSNITLTLNGLERTTKYTSYEDNFRDQFPPNFPYALLKSDS--EKE 292
Db 1249 KYNVSDSTNKHLETSPNLLKLEAEQAKQALEKKRLGLE-----SELKHVNEQLEEE 1302
QY 293 AKEKET-----LIIMTKTLDIVKVMVYKGTISPBEGVSYLE----- 329
Db 1303 KQKESNEKRVKVDLEKEVSELKDQIEEVASKAVTEAKNKESELDEIKROYADVSSR 1362
QY 330 --NLDSMIALQTKN-KLEKNATDNISKLPAPSEKSHETD-----STKEEAKEKEY 380
Db 1363 DKSVEQLTKLOAKNEELRTAEAEQOLDRAERSKKAFFDLEEAVKNELEETAKKVKAE 1422
QY 381 GSKLSTKDDNSPNPGKTDPEKGTKEAYLEAIRKNIEWLKHKDKGNKEDYDLKMRDFI 440
Db 1423 KAMKKAETDYRSTKSELDAKNVSSQYVQIKRLNEE-----LSELSVL 1467
QY 441 NKQADAYVEKGLDKKEAEA 460
Db 1468 --EADERCNSAIKAKKTAES 1486

RESULT 5

RA50_PYRFU STANDARD; PRT; 882 AA.
AC P58301;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR PF1167.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RX MEDLINE=20485553; PubMed=11029422;
RA Hopfner K.-P., Karcher A., Shin D., Fairley C., Tainer J.A.,
RA Carney J.P.,
RA "Mrell and Rad50 from Pyrococcus furiosus: cloning and biochemical
RT characterization reveal an evolutionarily conserved multiprotein
RL machine.";
RL J. Bacteriol. 182:6036-6041(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RN Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 1-149.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RX MEDLINE=20348838; PubMed=10892749;
RA Hopfner K.-P., Karcher A., Shin D.S., Craig L., Arthur L.M.,
RA Carney J.P., Tainer J.A.;
RT "Structural biology of Rad50 ATPase: ATP-driven conformational
RT control in DNA double-strand break repair and the ABC-ATPase
RT superfamily.";
RL Cell 101:789-800(2000).
CC -I- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mrell complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mrell by unwinding
CC and/or repositioning DNA ends into the mrell active site.

CC -I- SUBUNIT: Forms a complex with mrell.
CC -I- SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE010225; AAL81291.1; -
DR PDB; 1F2T; 20-SEP-00.
DR PDB; 1F2U; 02-AUG-00.
DR PDB; 1I18; 30-MAY-01.
DR PDB; 1L8D; 28-AUG-02.
DR HAMAP; MF_00449; -; 1.
DR InterPro; IPR003439; ABC-transporter.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF04423; Rad50_zn_hook; 1.
DR Pfam; PF02463; SMC_N; 1.
DR ProDom; PD000006; ABC-transporter; 1.
KW DNA repair; Hydrolase; ATP-binding; Coiled coil; 3D-structure;
KW Complete proteome.
FT NP_BIND 30 37 ATP.
FT DOMAIN 148 744 COILED COIL (POTENTIAL).
SQ SEQUENCE 882 AA; 103839 MW; 3ADCBD250382A99E CRC64;

Query Match 7.5%; Score 181; DB 1; Length 882;
Best Local Similarity 21.0%; Pred. No. 0.082;
Matches 119; Conservative 99; Mismatches 186; Indels 164; Gaps 23;

QY 29 KSLNHR-----ELSAERPLNEOIAEAED-----KIKKTYPPENKPGOSNFFVD 73
Db 178 KTNNRIKEYRDILARTENIEELIKENEQELIOVLEISKIEVLP-----SKRSKVD 230
QY 74 NL--NLLRAITEKEKIEKERSIRSSPLONKLNVEDVDST-----KNRKL---IDD 119
Db 231 MLRKEVLEETKVEITENSERLEKRRGDKRTLEERIKNTEEYLEKLEKEKELEQVKE 290
QY 120 YDSTKSGLD-----HKFQDD-PDGLHQDGTPLTAEDIVHIAIRYE----- 161
Db 291 ITSIKKDVDAYLALKEFKNEYLDKYIEKELTRVEELINEIQRIEELNEKESEKEKLE 350
QY 162 -----ENDRAVFDKIVSKLLNLGLITESQAHTLEDEVAEVLQKLIKESEKLE 208
Db 351 NEKKEILNLAILEKHQHYEELKAKKENLRQLKEKLGDKSPEDIKKLELEETKK-TTI 409
QY 209 EEDPNKPTSWENOGAKIPEKVTMAAIOQDL--AKGE-----NDETVSNTL----- 253
Db 410 EERNEIT-----QRIGELKNKIGDLKTAIELKAKGKPCVCGRELTDREHRELLSKYHL 465
QY 254 -----TLTNGLERTKTYSE-----DNFRDQYFFNFYALLKSID 288
Db 466 DLNNSKNTLAKLDIRKSELELRIDMETIKRTPLLTVAEQIRSEELNLYNLEK--- 522
QY 289 SEKEAKEKETLITMTLIDFVKVMVYKGTISPBEGVSYLENDEMA--LOTNKNLEKN 346
Db 523 IEKNATEYKLEELRTLEGRIRGLA-----EDLKLAPLEKKLALIHKKQLEKE 574
QY 347 ATDNISKLPAPSEKSHETDSTKEEAKEKEYSLKSDTKD-----DNSNPGGK 397
Db 575 LKELNTKL-ESFGFKSVEDLSKLELEIYKRYLTLLNSKKELEITQREIAKAKETLEM 633
QY 398 TDEPKGKTEAYLEAIRKNIEWLKHKDKGNKEDY-----DLSK 435
Db 634 SFEEAEVEADIERIEKLSQLK---QKYNEEYKKKREKEKEKELARLEAQKKELEK 690
QY 436 MRDFINKQADAYVEKGLDKKEAEAIAKR 463
Db 691 RRDITK-----STLEKLAKEENRERVKK 714

RESULT 6		SQ SEQUENCE 1790 AA; 206424 MW; 6CE2B216E9FD4818 CRC64;	
ID	USOL_YEAST	STANDARD;	PRT; 1790 AA.
AC	P25386;	Query Match 7.5%; Score 181; DB 1; Length 1790;	
DT	01-MAY-1992 (Rel. 22, Created)	Best Local Similarity 19.9%; Pred. No. 0.19;	
DT	01-MAY-1992 (Rel. 22, Last sequence update)	Matches 118; Conservative 102; Mismatches 176; Indels 196; Gaps 28;	
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Intracellular protein transport protein USOL.		
DE	USOL OR INT1 OR YDL058W.		
GN	Saccharomyces cerevisiae (Baker's yeast).		
OS	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.		
OC	NCHI_TaxID=4932;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	STRAIN=X2180-1A;		
RC	MEDLINE=91185402; PubMed=2010462;		
RX	Nakajima H., Hirata A., Ogawa Y., Yonehara T., Yoda K.,		
RA	Yamasaki M.;		
RT	"A cytoskeleton-related gene, usol, is required for intracellular		
RT	protein transport in Saccharomyces cerevisiae.";		
RL	J. Cell Biol. 113:245-260(1991).		
RL	[2]		
RP	SEQUENCE OF 782-1790 FROM N.A.		
RA	Hendrick K.E.; Herman D.J.; Bendel C.M.; McClellan M.; Tao N.,		
RA	Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RP	SEQUENCE OF 1-8 FROM N.A.		
RA	Bai Y., Symington L.S.;		
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE ER TO THE GOLGI		
CC	COMPLEX.		
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSOCIATED WITH INTRACELLULAR		
CC	MEMBRANES. PROBABLY PRESENT ON VESICLES OPERATIONAL BETWEEN THE		
CC	ER AND THE GOLGI COMPLEX.		
CC	-1- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED		
CC	OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL		
CC	COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.		
CC	-1- SIMILARITY: BELONGS TO THE VDP/USOL/YBL047C FAMILY.		
CC			
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CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC			
DR	EMBL; X54378; CAA38253.1; -		
DR	EMBL; L03188; AAB00143.1; -		
DR	EMBL; U53668; AAB66659.1; -		
DR	SGD; S0002216; USOL.		
DR	InterPro; IPR002017; Spectrin.		
DR	InterPro; IPR006955; Usol_p115_c.		
DR	InterPro; IPR006953; Usol_p115_head.		
DR	Pfam; PF04871; Usol_p115_C; 1.		
DR	Pfam; PF04869; Usol_p115_head; 1.		
KW	Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.		
FT	DOMAIN 1 724		
FT	DOMAIN 725 1790		
FT	DOMAIN 465 487		
FT	DOMAIN 991 1790		
FT	DOMAIN 1172 1786		
FT	CONFLICT 847 847		
FT	CONFLICT 924 924		
FT	CONFLICT 1253 1253		
FT	CONFLICT 1319 1319		
FT	CONFLICT 1461 1461		
FT	CONFLICT 1581 1581		
FT	CONFLICT 1600 1600		
FT	CONFLICT 1661 1661		
FT	CONFLICT 1772 1772		
FT	D -> DEEDDEE (IN REF. 2).		

RESULT 7		MAPB_MOUSE	
ID	MAPB_MOUSE	STANDARD;	PRT; 2464 AA.
AC	P14873;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-APR-1990 (Rel. 14, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))		
DE	[Contains: MAP1 light chain LC1].		
GN	MAP1B OR MTAP1B OR MTAP5.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A., AND DOMAIN.		
RC	STRAIN=Swiss Webster; TISSUE=Brain;		
RX	MEDLINE=90094539; PubMed=2480963;		
RA	Noble M., Lewis S.A., Cowan N.J.;		
RT	"The microtubule binding domain of microtubule-associated protein		
RT	MAP1B contains a repeated sequence motif unrelated to that of MAP2		
RT	and tau.";		
RL	J. Cell Biol. 109:3367-3376(1989).		
CC	-1- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.		
CC	PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES		
CC	THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST		

DR Pfam: PF05062; RICH; 1.
DR Pfam: PF04650; YSRK.Signal; 1.
DR ProDom: PD153432; Csurface_antigen; 1.
DR SMART: SM00409; IG; 1.
DR TIGRFAMS: TIGR01167; LPXG_anchor; 1.
DR TIGRFAMS: TIGR01168; YSRK.Signal; 1.
DR PROSITE: PS00847; GRAM_POS_ANCHORING; 1.
DR PROSITE: PS00835; IG.LIKE; FALSE_NEG.
KW Cell wall; Peptidoglycan-anchor; Receptor; Repeat; Signal;
KW Immunoglobulin domain.
FT SIGNAL 1 37
FT CHAIN 38 1135 IGA FC RECEPTOR.
FT PROPP 1136 1164 REMOVED BY SORTASE (POTENTIAL).
FT DOMAIN 434 534 IG-LIKE.
FT DOMAIN 199 438 IGA-BINDING (POTENTIAL).
FT DOMAIN 439 826 IGA-BINDING (POTENTIAL).
FT DOMAIN 827 945 PRO-RICH REPEATS.
FT SITE 1132 1136 LPXG SORTING SIGNAL (POTENTIAL).
FT MOD_RES 1135 1135 AMIDE-LINKED TO CELL WALL (POTENTIAL).
FT SEQUENCE 1164 AA; 131051 MW; 65DE94AF720A5474 CRC64;

Query Match 7.1%; Score 169.5; DB 1; Length 1164;
Best Local Similarity 21.4%; Pred. No. 0.41;
Matches 123; Conservative 78; Mismatches 189; Indels 185; Gaps 25;

QY 36 LSAERPLN-----QIAAEEDKIKKTPPENKPGOSYFVDNLLRAIT-EKEK 86
DB 149 LELEQFNTRNLLHITKQHEVEKKKAK-----QKTLKQSDTKVDLSNIDELNHNKQSQ 204

QY 87 IEK--ERQSIRSPDNKL-----NVEDVSTNKRKLIDYDSTKGLDHK 130
DB 205 VKMAEQKGTITNEDKDSMLKTIKQQAQADKEDAEVKEELKGLFSSTKAGLDQE 264

QY 131 FQDDPGLHOLDGTPITAEDIVHKI-----AARIYENDRAVDKIVSKLLNLG 179
DB 265 IQE-----HVKKET--SSEENTQKDEHYANSLQNLQAOKSLEELDKATTNEQATQVKNOF 317

QY 180 L-----ITESAHTLEDEVAEV-----LQKLSKE---ANNYEE 210
DB 318 LENAQKLKEIOLPIKETNVKLYKANSELEQVEKELKHNSLEANLEDLVAKSKEIVREYEG 377

QY 211 DPNKPSWTE-----NQAKIPEKTPMAAIOGLAKGENDPTVSN 251
DB 378 KLNQSKNLPOLKEBEAHSKLVQVVEDEFKFKFTSEQVTPKRVKRDIAANENNQ---Q 434

QY 252 TLTLTNGLERRYKTYSEDFRQFPNFPYALLKSIDSEKAEKETLITIMKLILDFVK 311
DB 435 KIETVSPENITVYEGED-----VKFTVTAKS-DS-----KTTLDLDFSD 471

QY 312 MMVKG-TTSPGVSYLENLD-----EMIALQTK---NKLEKNATD 349
DB 472 LTKYNPVSVDRISTNYKNTDNHKTAEITIKNLKNSQTVTLKAKDDSGNVVEKFTFI 531

QY 350 NISKLPAPSEKSHETDSTKEAA-----KMEKEYGSLKD 385
DB 532 TVQKKEEKQVPTPEQKDSKTEKVPQEPKSDKNQOLIKLSAQOQLEKLEKAIKELME 591

QY 386 STKDDNSNGGKDEPKGTEYALEAIRNIEWLK-----HDKGKNKEDYDLSKMRDFTN 441
DB 592 Q-PEIPSNP--EYGIQKSWESQKEPIQEAITSFKKIIIGDSSSKYKTYEYFNKRYKSDFMN 648

QY 442 KQADAVVEKGILDKAE-----AIKRIYSS 467
DB 649 YQLHAQW--MLTRKVVQYMNKYPDNAEIKKIFES 681

RESULT 10
ID REST_HUMAN STANDARD; PRT; 1427 AA.
AC P30622;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed-
Sternberg intermediate filament associated protein).
GN RSN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood monocytes;
RX MEDLINE=92289675; PubMed=1600942;
RA Bilbe G., Delabie J., Brueggen J., Richener H., Asselbergs F.A.M.,
RA Cerletti N., Sorg C., Odink K., Tarcsay L., Wiesendanger W.,
RA de Wolf-peeters C., Shipman R.;
RT "Restin: a novel intermediate filament-associated protein highly
RT expressed in the Reed-Sternberg cells of Hodgkin's disease.";
RL EMBO J. 11:2103-2113(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92405160; PubMed=1356075;
RA Pierre P., Scheel J., Rickard J.E., Kreis T.E.;
RT "CLIP-170 links endocytic vesicles to microtubules.";
RL Cell 70:887-900(1992).
CC -!- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED PROTEIN
CC THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
CC CYTOSKELETON.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name-Long;
CC IsoID=P30622-1; Sequence-Displayed;
CC Name-Short;
CC IsoID=P30622-2; Sequence-VSP_000765;
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE REED-STERNBERG CELLS
CC OF HODGKIN'S DISEASE.
CC -!- SIMILARITY: Contains 2 CAP-Gly domains.
CC -----
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CC -----
DR EMBL: X64838; CA446050.1; -;
DR EMBL: M97501; AAA35693.1; -;
DR PIR: S22695; S22695.
DR Genew: HGNC:10461; RSN.
DR MIM: 179838; -;
DR GO: GO:0005768; C:endosome; TAS.
DR GO: GO:0005882; C:intermediate filament; TAS.
DR GO: GO:0015630; C:microtubule cytoskeleton; TAS.
DR GO: GO:0008017; F:microtubule binding activity; TAS.
DR GO: GO:0006899; P:non-selective vesicle transport; TAS.
DR InterPro: IPR000938; CAP-Gly.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF01302; CAP_GLY; 2.
DR SMART: SM00343; Znf_C2HC; 1.
DR PROSITE: PS00845; CAP_GLY_1; 2.
DR PROSITE: PS0245; CAP_GLY_2; 2.
DR Cytoskeleton; Microtubules; Coiled coil; Repeat; Alternative splicing.
KW DOMAIN 78 120 CAP-GLY 1.
FT DOMAIN 143 204 SER-RICH.
FT DOMAIN 232 274 CAP-GLY 2.
FT DOMAIN 304 331 SER-RICH.
FT DOMAIN 350 1342 COILED COIL (POTENTIAL).
FT DOMAIN 1408 1421 CCHC-BOX.
FT VARSPIC 457 491 Missing (in isoform Short).
FT CONFLICT 1069 1069 D -> E (IN REF. 2).
FT SEQUENCE 1427 AA; 160989 MW; 0A4F166DD94254E8 CRC64;
SQ

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Query Match 7.1%; Score 169.5; DB 1; Length 1427;
Best Local Similarity 22.0%; Pred. No. 0.52;
Matches 109; Conservative 79; Mismatches 184; Indels 123; Gaps 20;

Oy 34 RELSAE-----RPLNEQIAAEEDKIKKTYPPENKPGOSNYSFVDNL-----NLRA 80
Db 769 KASSEGSEKMKLQQQL-EAAEKQIKHLEKNAESSKASITRELOGRELKTNQEN 827
Oy 81 ITE-----REKIEKERQ-----SIRSSPLD-----NVEDVDSTKN 113
Db 828 LSEVSQVETLEKELQILKEFAEASEAVSORSQETVKNLHQKEQFNMSSLDLEKL 887
Oy 114 RKLDDYSTKSLDHHKQDDPDGLHQLDGLTPLAEDIVHKAARIYEENDRAVDFKTVS 173
Db 888 RENLAD-----MEAKFERKDEREQL-----IKAKEKLEND-----IA 920
Oy 174 KLLNLGLITESQAHTLEDEV-----AEVLQKLISKEANNYE-----EDPKPTISWTEN 221
Db 921 EIMKSGNSQOLTKMDELRLKERDVEELQKLTKANENASFLOKSTEDMTVRAEOSQ 980
Oy 222 QAGKIPEKVTMAAIIQDGLAKGENDETVSNLTTLTNGLERRTKTYSEDNFRDFQVFPNFY 281
Db 981 EAARKHEE-----EKKELEKRLSD-----LEKKMET-SHNOQCELEK-----1015
Oy 282 ALLKSIDSEKAKKETLITITMTKLIDPVKMMVKYGTISPEEGVSYLENLDEMIALQTKN 341
Db 1016 ARYERATSETTKHEEILQNLQKLTILDTEDLKG-----ARENSGLLQLEELRQADKA 1071
Oy 342 KLEKNATDNISKLPAPSEKSH--EETDSTKEEAKEKVEGSLKDKSTKDNPNPGKTD 399
Db 1072 KAAQTAEDAMQIMQMTKEKTETTLASLDTTKQTNKQLQNLDELTLKENNL-KNVEBELNKS 1130
Oy 400 EPGKTEAYLEAIRKNIEWLKHH-----DKGNKEDYDLKMRDFINKQADAYV 448
Db 1131 ELLTVENQKMEERKEIETLQAAAKSQOALSALQEEVKNLAELGLSRDVTSHQKLEE 1190
Oy 449 EKGILDKEEAIRK 463
Db 1191 ERSVLNQLLEMKKR 1205

RESULT 11
RA50_METJA STANDARD; PRT; 1005 AA.
AC Q58718;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA double-strand break repair rad50 ATPase.
GN RAD50 OR MJ1322.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RA jannaschii".
RL Science 273:1058-1073(1996).
CC -1- FUNCTION: Involved in DNA double-strand break repair (DSBR). The
CC rad50/mre11 complex possesses single-strand endonuclease activity
CC and ATP-dependent double-strand-specific exonuclease activity.
CC Rad50 provides an ATP-dependent control of mre11 by unwinding
```

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RBP2_PLAVB          STANDARD;          PRT; 1251 AA.
ID  RBP2_PLAVB          STANDARD;          PRT; 1251 AA.
AC  Q00799;
DT  01-APR-1993 (Rel. 25, Created)
DT  01-APR-1993 (Rel. 25, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Reticulocyte binding protein 2 (Fragment).
GN  RBP2.
OS  Plasmodium vivax (strain Belem).
OC  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX  NCBI_TaxID=31273;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=92315338; PubMed=1617731;
RA  Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
RT  "A reticulocyte-binding protein complex of Plasmodium vivax
RT  merozoites";
RL  Cell 69:1213-1226(1992).
CC  -!- FUNCTION: INVOLVED IN RETICULOCYTE ADHESION. SPECIFICALLY BINDS TO
CC  HUMAN RETICULOCYTE CELLS.
CC  -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  EMBL; M88098; AAA29744.1; -.
DR  Malaria; Receptor; Membrane.
KW  NON_TER 1
FT  NON_TER 1251
SQ  SEQUENCE 1251 AA; 143741 MW; 54BA51C7404AC572 CRC64;

Query Match          7.0%; Score 168; DB 1; Length 1251;
Best Local Similarity 20.3%; Pred. No. 0.52;
Matches 100; Conservative 95; Mismatches 178; Indels 120; Gaps 23;

QY  27 QDKSLNRELRAER---PLNEQIAEAEEDKIKTYPPENKPGQSNYS--FVD-NLNLRA 80.
DB  8 KOTSFDEKKKSIEKAYKMGNTLKELEKMDDEKIEVEEAQIQYKRFIDHVNLMND 67
QY  81 ITEKIEKEROSIRSPDL---NKLNVEDVDSTKNRKLDDYDS-----122
DB  68 EVEKSLVMEKELYKEDEIKQKNEYKQGDTSNFYTYEQYNSATQSKAKIEQFINIA 127
QY  123 -TKSGLDHFKPD-----DPDGLHQLDGTPLTAEDIV-----HKIA 156
DB  128 TTKKGTSDTSQDINELESIEKEVHKVLQLVKQESNMEEMRKQILSMKDLILNNSETIA 187
QY  157 ARI-----YEENDRAVDFKIVSKLIN--LGLITESQAH-----TLED-----EVA 194
DB  188 KEISNNQNALGFRENKATKLNK--TDELLQRAVAAIEEAKAHKNNDIALEDAQIDTEYS 246
QY  195 EVLOKLIKEANNYEDPNKPTSWENQAGKIPEKVTPTMAAIOODGLAKEG---NDETVS 250
DB  247 KIEQ--INREIMNKKDEIKSYLSEIKYKDKCTTEISNKRKDKLEFLEKFKPNESNS 304
QY  251 NTLTLNGLERRTKTYSDFNDFQVFPNFIALLKSI-DSEKAEKKEKTLITIMKTLIDF 309
DB  305 NKNVINE-----INENIRNSEQY-----LKDIEDAEKQASTK-----336
QY  310 VKMWKYGKITSPEGVSYLENDEMIALQTKNKLKNATDNITSLKFPAPSEKSHETDST 369
DB  337 VELFHKH-----ETTISNFKSEILGVETKSKKINKAEDIMKETERHNSETQTVKGF 391
QY  370 KEBAKMEKEYGLKSDTDDNSNPGCKTDEPKGKTEAYLEAIRKNIMELKKHDKKGNKE 429
DB  392 QENLNLKNEPHN--YDNAEDELNN--DKSTNAKVLJETNLNLSYKHNLSI-TNIKOGGEK 446
QY  430 DVDLSKMRDFINK 442

DB  447 IY--SKAKDIMQK 457

RESULT 13
TRDN_CANFA          STANDARD;          PRT; 700 AA.
ID  TRDN_CANFA          STANDARD;          PRT; 700 AA.
AC  P82179;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Triadin.
GN  TRDN.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX  TISSUE=Heart, and Skeletal muscle;
RX  MEDLINE=99428545; PubMed=10497235;
RA  Kobayashi Y.M., Jones L.R.;
RT  "Identification of triadin 1 as the predominant triadin isoform
RT  expressed in mammalian myocardium.";
RL  J. Biol. Chem. 274:28660-28668(1999).
CC  -!- FUNCTION: MAY BE INVOLVED IN ANCHORING CALSEQUESTRIN TO THE
CC  JUNCTIONAL SARCOPLASMIC RETICULUM AND ALLOWING ITS FUNCTIONAL
CC  COUPLING WITH THE RYANODINE RECEPTOR (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
CC  reticulum.
CC  -!- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=3;
CC  Name=Skeletal;
CC  IsoId=P82179-1; Sequence=Displayed;
CC  Name=Cardiac 1;
CC  IsoId=P82179-2; Sequence=VSP_004001, VSP_004002;
CC  Name=Cardiac 3;
CC  IsoId=P82179-3; Sequence=VSP_004003, VSP_004004;
CC  -!- TISSUE SPECIFICITY: SKELETAL AND CARDIAC MUSCLE.
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CC  or send an email to license@isb-sib.ch).
CC  EMBL; AF165916; AAF00222.1; -.
DR  EMBL; AF165915; AAF00221.1; -.
DR  EMBL; AF165917; AAF00223.1; -.
KW  Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
KW  Alternative splicing.
FT  INIT_MET 0 0 BY SIMILARITY.
FT  DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 47 67 POTENTIAL.
FT  DOMAIN 68 700 LUMENAL (POTENTIAL).
FT  CARBOHYD 74 74 N-LINKED (GLCNAC... ) (POTENTIAL).
FT  CARBOHYD 616 616 N-LINKED (GLCNAC... ) (POTENTIAL).
FT  VARSPLIC 257 277 DQYAFCRYMIDMFVHGDLRPG -> GKHSSEVAGSGKRTLG
FT  FTID=VSP_004001. KKOIQ (in isoform Cardiac 1).
FT  Missing (in isoform Cardiac 1).
FT  /FTID=VSP_004002.
FT  E -> EPIKGEVKVPGSLKEKE (in isoform
FT  Cardiac 3).
FT  /FTID=VSP_004003.
FT  EEKVKQVKEATEKAATEKTVKPKAKAHOEKESPTIKTD
FT  KPRTSKETPEVTES -> GILQVVPVNLCLFLVQFQDE
FT  ELNVEKVFMRHIVLSHPTSRTSPILVISTCRT (in
FT  isoform Cardiac 3).
FT  /FTID=VSP_004004.
FT  SEQUENCE 700 AA; 78152 MW; F033E3AA1BEE0C56 CRC64;
SQ
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QY 269 DNFDFQYPPNFYALKSI-----DSEKAEKETLITIMKTLLIDFVMMVKY 316
Db 589 -----LYISKMKSEVSLVNRSKQLESQMSNRKNMNASRELAACQLLISOHEAKIKS 642
QY 317 GRISPEEGVSYLENDETALQTKNLEK---NATDNISKLPAPSEKSHETDSTKE-- 371
Db 643 LT-----DYQNMNE-----QRRKQLESQDLSLSELAKL--RAQEKHVEYSFQDKEKE 688
QY 372 -----EAAKMEKESGLSKDTKDDNSNPGGTDPRKGTAYLAIRKNIEWLKHKDKK 425
Db 689 HLTRLODAEMKALQEQMESUREAHQKLSRLRDEIEKQKIIDEIRLQKLEQEK 748
QY 426 GNKEDYDLSKMRDFINKQADAYVEKIL--DKEE 457
Db 749 -LSSDYNKLIKIED---QEREMKLEKLLLLNDKRE 778

RESULT 15
CENE_HUMAN STANDARD; PRT; 2663 AA.
AC Q02224;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Centromeric protein E (CENP-E protein).
GN CENPE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP MEDLINE-93024922; PubMed-1406971;
RA Yen T.J., Li G., Schaar B.T., Szilak L., Cleveland D.W.;
RT "CENP-E is a putative kinetochore motor that accumulates just before
RT mitosis.";
RL Nature 359:536-539(1992).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE-95196755; PubMed-7889940;
RA Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;
RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed
RT microtubule motor.";
RL EMBO J. 14:918-926(1995).
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-98437347; PubMed-9763420;
RA Chan G.K.T., Schaar B.T., Yen T.J.;
RT "Characterization of the kinetochore binding domain of CENP-E reveals
RT interactions with the kinetochore proteins CENP-F and hBUBR1.";
RL J. Cell Biol. 143:49-63(1998).
CC -!- FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE
CC KINETOCHORE MOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE
CC OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT
CC AND/OR SPINDLE ELONGATION.
CC -!- SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.
CC -!- SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING
CC CONGRESSION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS
CC QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.
CC -!- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z15005; CAA78727.1;
CC FIR; S28261; S28261.
CC HSSP; P17119; 3KAR.
CC Genew; HGNC:1856; CENPE.

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DR GO; GO:0000067; P:DNA replication and chromosome cycle; TAS.
DR GO; GO:0007079; P:mitotic chromosome movement; TAS.
DR GO; GO:0007080; P:mitotic metaphase plate congression; TAS.
DR InterPro; IPR001752; kinesin_motor.
DR Pfam; PF00225; kinesin; 1
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DR SMART; SM00129; KISC; 1.
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KW Cell cycle; Centromere.
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ACCESSION	AF453583
VERSION	AF453583.1 GI:18265965
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SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
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REFERENCE	Rong,Y.P., Liu,F., Zeng,L.C., Ma,W.J., Wei,D.Z. and Han,Z.G.
AUTHORS	Cloning and characterization of a novel human secretory protein:
TITLE	secretogranin III

JOURNAL	Sheng wu hua hshueh yu sheng wu wu li hshueh pao 34 (4), 411-417 (2002)
MEDLINE	22093564
PUBMED	12098761
REFERENCE	2 (bases 1 to 3371)
AUTHORS	Rong, X., Liu, F. and Han, Z.
TITLE	Direct Submission
JOURNAL	Submitted (30-NOV-2001) Function Genome Department, Chinese National Human Genome Center, 351 Guo Shou-Jing Road, Shanghai 201203, P. R. China
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LOCUS AX092418 1893 bp DNA linear PAT 21-MAR-2001
DEFINITION Sequence 149 from Patent WO0116318.
ACCESSION AX092418
VERSION AX092418.1 GI:13444523
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Eaton,D.L., Pilvaroff,B., Gerritsen,M.E., Goddard,A.,
Gadowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0116318-A 149 08-MAR-2001;
Genentech, Inc. (US)
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RESULT 3
AX463956 1893 bp DNA linear PAT 16-JUL-2002
LOCUS
DEFINITION Sequence 89 from Patent WO0140466.
ACCESSION AX463956
VERSION AX463956.1 GI:21898995
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L., and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 89 07-JUN-2001;
Genentech Inc. (US)
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Best Local Similarity 99.7%; Pred. No. 0;

Matches 1870; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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RESULT 4

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BD127901
LOCUS
DEFINITION
ACCESSION BD127901
VERSION
KEYWORDS JP 2002017375-A/3332.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1871)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
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TITLE
JOURNAL
COMMENT
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 3332 22-JAN-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/3332
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
10,
PC C12P21/02,C12O1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1865; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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LOCUS Homo sapiens cDNA FLJ90833 fis, clone Y79AA1001803, highly similar
to Homo sapiens secretogranin III mRNA.
AK075314
ACCESSION AK075314.1 GI:22761322
VERSION oligo capping; fis (full insert sequence).
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Isoqai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
Kawai-Hio,Y., Saiko,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
Ninomiya,K.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1871)
AUTHORS Isoqai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (25-MAR-2002) Takao Isoqai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology; cDNA library construction:
Institute of Medical Science, University of Tokyo, Laboratory of
Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
sequencing and clone selection: Helix Research Institute (supported
by Japan Key Technology Center etc.).
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Best Local Similarity 99.7%; Pred. No. 0;
Matches 1865; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 6

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DEFINITION BC014539 Homo sapiens, clone MGC:13448 IMAGE:4283082, mRNA, complete cds.
ACCESSION BC014539
VERSION BC014539.1 GI:15778921
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1676)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbiology.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
 Greene, Mark Kettman and Anuradha Madan
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 19 Row: 1 Column: 10
 This clone was selected for full length sequencing because it
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FEATURES             Location/Qualifiers
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Query Match	80.9%	Score 1632.6;	DB 9;	Length 1676;	
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Qy	311	GGATTCCTGGTCTTAGTGTCTCCCGATTCAAGCTTTCCCAACCTTGGAGAAAGCAAGACA	370		
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Qy	551	AAGAAAGACAATCTATAGAAGCTCCCGACTTTGATATAAGATTGAATGTGAAGATGTGTG	610		
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QY	851	TGGAAGATGAAGTAGCAGAGTTTACAAAAATTAATCTCAAGAGAACCCACAAATTAAG	910
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QY	1211	TTGTGAAGATGATGGTGAATATGGAACAATATCTCCAGAAAGAGTGTTCCTACCTTG	1270
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Db 1914 TTTCTATATAGAACTCTTATTTCTTC-TTGAATTTTACATTTTGTATACAGAGATGCTG 1972

QY 1960 CTTTGGAAAA 1969

Db 1973 CTCTGGAAAA 1982

RESULT 8

MMSGIII

LOCUS MMSGIII 2163 bp mRNA linear ROD 07-DEC-1994

DEFINITION Mus musculus secretogranin III (SgIII) mRNA, complete cds.

ACCESSION U02982

VERSION U02982.1 GI:413763

KEYWORDS Mus musculus (house mouse)

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

2 (bases 1 to 2163)

Dopazo, A.

Direct Submission

TITLE

JOURNAL

Submitted (28-OCT-1993) Dopazo A., The Scripps Research Institute, Molecular Biology, 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

FEATURES

source

1. 2163

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VERGILDKEANAIKRIYSSL"

BASE COUNT 708 a 522 c 496 g 437 t

ORIGIN

Query Match 61.2%; Score 1235.4; DB 10; Length 2163;

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Matches 1596; Conservative 0; Mismatches 357; Indels 37; Gaps 11;

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Qy 1960 CTTTGGAAAA 1969
Db 1973 CTCTGGAAAA 1982

RESULT 9
RNSGIII

LOCUS RNSGIII 2146 bp mRNA linear ROD 07-DEC-1994
DEFINITION Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.
ACCESSION U02983
VERSION U02983.1 GI:413765
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
AUTHORS Dopazo, A., Lovenberg, T.W., Danielson, P.E., Ottiger, H.P. and Sutcliffe, J.G.
TITLE Primary structure of mouse secretogranin III and its absence from deficient mice
JOURNAL J. Mol. Neurosci. 4 (4), 225-233 (1993)
MEDLINE 95001263
PUBMED 7917832
REFERENCE 2 (bases 1 to 2146)
AUTHORS Dopazo, A.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1993) Dopazo A., The Scripps Research Institute, Molecular Biology, 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA
FEATURES
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Db 1974 TGCTCTTCTGGAAGA 1988

RESULT 10

BC024785

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BC024785 2175 bp mRNA linear ROD 16-APR-2003
Mus musculus secretogranin III, mRNA (cdna clone MGC:36181
IMAGE:5362975), complete cds.

BC024785 GI:19353444

MGC.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2175)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahney, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shreenikar, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smal, D.E.,

Schere, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED
22388257
REFERENCE
2 (bases 1 to 2175)
AUTHORS
Strausberg, R.
JOURNAL
Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT
Contact: MGC help desk
Email: cgabps-remail.nih.gov
Tissue procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E.-E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.-E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 53 Row: d Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677866.

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/db_xref="LocusID:20255"
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BASE COUNT

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RESULT 12
BD125387
LOCUS BD125387 799 bp DNA linear PAT 18-SEP-2002
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD125387
VERSION BD125387.1 GI:23220332
KEYWORDS JP 2002017375-A/818.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 799)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 818 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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PN JP 2002017375-A/818
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
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PI ISHII,
PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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CC C12P21/02,C12Q1/68/C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
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ACCESSION		BD108467
VERSION		BD108467.1 GI:23203285
KEYWORDS		JP 2002010789-A/544.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE		I (Bases 1 to 527)
JOURNAL		Edwards,J.B.D.M., Jobert,S. and Giordano,J.E. EST and encoded human protein Patent: JP 2002010789-A 544 15-JAN-2002; GENSET CORP
COMMENT		OS Homo sapiens (human) PN JP 2002010789-A/544 PD 15-JAN-2002 PF 07-AUG-2000 JP 2000280989 PR 05-AUG-1999 US 60/147499 PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC C12N1/21, RC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC C12N15/00 CC n=a, g, c or t Location/Qualifiers FH key Location/Qualifiers FT CDS 154..525 FT misc_feature 18..19. Location/Qualifiers 1..527 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
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Matches 512; Conservative		3; Mismatches 12; Indels 1; Gaps 1;
QY		828 CACAGAAAGCCAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAAT 887


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Db      360  TATCATGAAACACTGATTGACTTTGTGAAGATGATGGTGAATATGGACAAATATCTCC 419
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Db      420  AGAAGAGGTGTTTCTACCTTGAAAACCTTGGATGAAATGATTGCTTTTCAGACCAAAAA 479
QY      1308  CAAAGCTAGAAAATAATGCTACTGACAAATATAGCAAGCTTTTCCAGC 1355
Db      480  CARGCTAGAAAATAATGCTACTGACAAATATAGCAAGCTTTTCCAGC 527

RESULT 15
XLSGIII
LOCUS      X.laevis mRNA for secretogranin III.          linear   VRT 05-AUG-1996
DEFINITION X.laevis mRNA for secretogranin III.
ACCESSION  X92872
VERSION    X92872.1 GI:1483620
KEYWORDS   secretogranin III.
SOURCE     Xenopus laevis (African clawed frog)
ORGANISM   Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae;
            Xenopodinae; Xenopus.

REFERENCE
AUTHORS    Holthuis, J.C. and Martens, G.J.
TITLE      The neuroendocrine proteins secretogranin II and III are regionally
            conserved and coordinately expressed with proopiomelanocortin in
            Xenopus intermediate pituitary
JOURNAL    J. Neurochem. 66 (6), 2248-2256 (1996)
MEDLINE    96217355
PUBMED     8632145
REFERENCE  2 (bases 1 to 2036)
AUTHORS    Holthuis, J.C.M.
TITLE      Direct Submission
JOURNAL    Submitted (07-NOV-1995) J.C.M. Holthuis, KUN, Dept. Animal
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CDS

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Db      392  GATAAGATGTTACACAAACAGGGAGTTAAGTGAAGAGAGACCTCTGGAAGAACAAGATT 448
QY      427  GAAGCAGAGAAGAAGAAATTAATAAACATATCTCCAGAAAACCAAGCCAGCTCAGAGC 486
Db      449  ---GCAGAGCGACACACTCTGACGAGCGCACAAAGCACAGAAAACCAAGAGATGCTTAA 505
QY      487  AACTATTCTTTTGTGATAACTTGAACCTTGCTGAAGGGCAATACAGAAAAGGAAAAAAT 546
Db      506  AATGATTCTTTTGGCGGATGATCTTGGGTTTTCGTCAATGGGAGAAAAAGATGTGAT 565
QY      547  GAGAAAAGAGACAATCTATAAGAAGCTCCCACTTTGATAATAAGTTGATGTGGAGAT 606
Db      566  GTCAAGAGAGAGTGGAGACCAAGAGGCTCTTTGGTAGTAACAGAGGTACCCCTGGATG 625
QY      607  GTTGATTCAACCAAGAAATCGAAAACCTGATCGATGATTATGACTCTTAAAGACTGGATG 666
Db      626  GCTGATTCAACCAAGAACTAAAGCTTGTGTAGTATTTTGATACCACTAAAGCATGCCG 685
QY      667  GATCATAAATTTCAAGATGATCCAGTGTCTTTCATCACTCACTGACGGGACTCCTTTAAC 726
Db      686  GATTATAAATATGAAGATGATCCTGATGCTTACACCACTTAATTCCTATGAGGCTAAAC 742
QY      727  GCTGAAGACATTTGCCATAAATCGCTGCCAGGATTTATGAAGAAAATGACAGAGCCGTG 786
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Db      923  CGTGAAGAGAGAGCAGGAGATCTGGATTTATTCAGACGTGA-----GATCAGACGTCTAT 976
QY      967  GAGAACTCAGCTCCCAATGCGACCAATTCAGATGCTTCTTAAGGAGGAGAAACAGATGA 1026
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QY      1027  ACAGATATCTAACACATTAACCTTGACAAAATGGCTTGGAAAGGAGAACTAAAACTACAT 1086
Db      1037  TCTGAACAAAAAACAAGAGATTTCTTTGACACTGTGAGAGAGAGGACCAATATATCTCT 1096
QY      1087  GAAGACAACTTTAGGAGCTTCCAATATTTCCCAAAATTTCTATGCGCTACTGAAAAATAT 1146
Db      1097  GAAGA-----TGATCTCCAGTATTTTCCCAAAATTTTAATCGACTTGTGAAAAAGCCTT 1147

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Search completed: August 28, 2003, 07:18:42
Job time : 7278 secs

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KW	Signal:	Cleavage	on pair of	basic residues; Polymorphism.
FT	SIGNAL	1	19	POTENTIAL
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FT	VARIANT	135	135	S -> N (in dbSNP:2305710).
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FT	CONFLICT	79	79	K -> R (IN REF. 1).
FT	CONFLICT	167	167	A -> V (IN REF. 1 AND 2).
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121	QY	121	DSTSGSLDHPQDDP	DGHL	DGTLPTA	EDIVHKIAARIYEENDRAVDFKIVSKLLNLGL	180	
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181	QY	181	ITESQAHTLEDEVA	EVLOKLI	SKAANNYEDPNKPT	SWTENQAGKIPEKVTMPMAIOQGL	240	
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241	QY	241	AKGNDETVSNTLT	TLNGLERR	TKTYS	EDNFRDFOYFPNFYALLKSIDSEKAKEKETLI	300	
241	Db	241	AKGNDETVSNTLT	TLNGLERR	TKTYS	EDNFRDFOYFPNFYALLKSIDSEKAKEKETLI	300	
301	QY	301	TIMKTLIDFVKMV	KVYGT	ISPEGVSYLENL	DEMIALQTKNKLKNATDNISKLPAPSE	360	
301	Db	301	TIMKTLIDFVKMV	KVYGT	ISPEGVSYLENL	DEMIALQTKNKLKNATDNISKLPAPSE	360	
361	QY	361	KSHEETDSTKEEA	AKMEKEVGS	LKSDT	DDNSNPGKTD	DPKGKTEAYLEAIRKNKIEWLK	420
361	Db	361	KSHEETDSTKEEA	AKMEKEVGS	LKSDT	DDNSNPGKTD	DPKGKTEAYLEAIRKNKIEWLK	420
421	QY	421	KHDKKGNKEDYD	L	SKMRDFT	NKQADAY	VEKGILDKEEAFAIKRIYSSSL	468
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AC	P47867;		
DT	01-FEB-1996	(Rel. 33, Created)	
DT	01-FEB-1996	(Rel. 33, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	Secretogranin III precursor (SgIII).		
GN	SCG3.		
MS	Mus musculus (Mouse).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus		
NCBI TaxID=10090;			

Query Match 87.2%; Score 2093.5; DB 1; Length 471;
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Matches 414; Conservative 17; Mismatches 37; Indels 3; Gaps 1;

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1	MGFLWTGWIILVLVNSGP	IQAFPPKPGSQDQSLNHNRELSAERP, LNEQIAEAEADIKKA	60
	QY	: : : : : : : : : : : : : : :	
58	YPPEKNKPGQSNYSFYDNLNLLRAIT	KEKIEKEROSIRSSPDNKLNVEDVDSTNKKLI	117
	Db	: : : : : : : : : : : : : : :	
61	PPSESKPSESNSYSDNLNLLRAIT	KEKIEKERSIRSPFDNQLNVEDAUSTNKKLI	120
	QY	: : : : : : : : : : : : : : :	
118	DDYDSTKSGLDHKFODDPDGLHQLDGT	PLTAEDIVHKIAARTYBENDRAVFDKYSKLEN	177
	Db	: : : : : : : : : : : : : : :	
121	DEYDSTKSGLOHKFODDPDGLHQLDGT	PLTAEDIVHKIATRIYENDRGVFDKYSKLEN	180
	QY	: : : : : : : : : : : : : : :	
178	LGLITESQAHTLEDEVAFLVKLISKE	NNYEDPNKPTSTWENQAGKIPKVT, PMAATQ	237
	Db	: : : : : : : : : : : : : : :	
181	LGLITESQAHTLEDEVAALOKLISKE	NNYEETLDKPTSTWENQDGKIPKVT, PVAAVQ	240
	QY	: : : : : : : : : : : : : : :	
238	DGLAGENDETVSNPLTITUNGLER	KTKTYSSEDNFRDQYFPNFYALLKSIDSEKEAKBE	297
	Db	: : : : : : : : : : : : : : :	
241	DGFTNRENDETVSNPLTISNGLERN	TNPHREDDFEELQYFPNFYALLTSIDSEKEAKE	300
	QY	: : : : : : : : : : : : : : :	
298	TLITIMKTLIDFVKMWVKYGTISPE	GYSYLENDEMIALQTKNKLKNATDNISKLPFA	357
	Db	: : : : : : : : : : : : : : :	
301	TLITIMKTLIDFVKMWVKYGTISPE	GYSYLENDETTALQTKNKLKNTTDSKSLPFA	360
	QY	: : : : : : : : : : : : : : :	
358	PSEKSHEETDSTKEEAARKWEKEY	GLSKDSTKDDNSNPGKGTDEPKGTKEAYLEARKNIE	417
	Db	: : : : : : : : : : : : : : :	
361	PPESQSHEETDSTKEEAARKWEKEY	GLSKDSTKDDNSNLGGKTDGATGKTEAYLEARKNIE	420
	QY	: : : : : : : : : : : : : : :	
418	WLKHKHKKGNKEDYDLSKMRDFIN	KQADAYVEYKGLDKEEAABAKRIYSSL	468
	Db	: : : : : : : : : : : : : : :	
421	WLKHKHKKGNKEDYDLSKMRDFIN	QADAYVEYKGLDKEEANAKRIYSSL	471
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RESULT 3	SG3_RAT	SG3_ID	SG3_RAT	STANDARD;	PRT;	471 AA.
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	DT		01-FEB-1996	(Rel. 33, Created)		
	DT		01-FEB-1996	(Rel. 33, Last sequence update)		
	DT		28-FEB-2003	(Rel. 41, Last annotation update)		
	DT		Secretogranin III precursor	(SgIII) (1B1075).		
	GN		SG3.			

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 Db 361 TTTCCCAACACCTGGAGGAGCCCAAGACAAATCTCTACATAATAGAGAATTAAGTGCAGA 420
 QY 402 AAGACCTTTGAGTGAACAGAGATTGCTGAAGCAGAGAGCAAGATTAAAAAATATATCC 461
 Db 421 GAGACCTTTGAGTGAACAGAGATTGCTGAAGCAGAGAGCAAGATTAAAAAATATATCC 480
 QY 462 TCCAGAAACCAAGCCAGGTCAGAGCAACTATTCTTTGTTGATAACTTTGAACCTGCTTAAG 521
 Db 481 CTCAGAAACCAAGCCAGGTCAGAGCAACTATTCTTTGTTGATAACTTTGAACCTGCTTAAG 540
 QY 522 GGCATTAACAGAAAGGAAAGAAATTTGAGAAAGAAAGCAATCTATAGAGAGCTCCCACT 581
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 QY 1842 ACATAGTCTTCTTCCGCTTAAACACTTCTGAAA-CTAAAGTTGTATGTAAGCTGAGATT 1900
 Db 1855 ATAGAGCTCTCTGCTCAATACACCTTATGAAGGTAAGTTGTAAGAGCTCGGTTT 1914
 QY 1901 TGTATACAG-----GAATCCTTATTTCTCATAGCTTATTTATTTATTCAGGAATA 1954
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 QY 1955 TGTGCTTTTGGAAA 1969
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RESULT 10 BC024785

LOCUS BC024785 2175 bp mRNA linear ROD 16-APR-2003
 DEFINITION Mus musculus secretogranin III, mRNA (cdna clone MGC:36181
 IMAGE:5362975), complete cds.

ACCESSION BC024785

VERSION BC024785.1 GI:19353444
 KEYWORDS MGC.

SOURCE ORGANISM

Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE AUTHORS

1 (bases 1 to 2175)
 Strausberg, R.D., Collins, F.S., Wagner, L.H., Derge, J.G.,
 Klausner, R.D., Fink, E.A., Grouse, L.H., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B.S., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

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RESULT 9
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Query Match
Best Local S
Matches 1584

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Qy	1
Db	1
Qy	1
Db	1
Qy	2
Db	2
Qy	2

RNSGIII 2146 bp mRNA linear ROD 07-DEC-1999
Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.
U02983
U02983.1 GI:413765

Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Rattus.

Dopazo, A., Lovenberg, T.W., Danielson, P.E., Ottiger, H.P. and
Sutcliffe, J.G.
Primary structure of mouse secretogranin III and its absence from
deficient mice
J. Mol. Neurosci. 4 (4), 225-233 (1993)

95001263
7917832
2 (bases 1 to 2146)
Dopazo, A.
Direct Submission
Submitted (28-OCT-1993) Dopazo A., The Scripps Research Institute,
Molecular Biology, 10666 N. Torrey Pines Rd., La Jolla, CA 92037,
USA

Location/Qualifiers
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691 a 523 c 496 g 436 t

Ch 60.6%; Score 1221.6; DB 10; Length 2146;
Similarity 79.4%; Pred. No. 2.2e-250;
884; Conservative 0; Mismatches 370; Indels 41; Gaps 10;

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